

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:45:41 ; Search time 182 Seconds
(without alignments)
2841.201 Million cell updates/sec

Title: US-09-516-728A-4
Perfect score: 7030
Sequence: 1 MKPARAPARLPSPRSGLRWA.....TIYENLAPVTTFKNGYIA 1337

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7030	100.0	1337	7	ADL16193 Human pro
2	7030	100.0	1337	8	ADP74603 Amino aci
3	6950	98.9	1337	7	ADL16195 Human pro
4	6824	97.1	1337	2	AAK85203 huDEP-1.
5	4508.5	64.1	1238	7	ADL16198 Mouse pro
6	4499.5	64.0	1216	7	ADL16200 Rat. prote
7	1811	25.8	341	8	ADP74604 Amino aci
8	1259.5	17.9	1998	8	AAO24268 Murine va
9	1242	17.7	1997	3	AAH19774 Human pro
10	1242	17.7	1997	4	AAH78821 Human pro
11	1242	17.7	1997	8	ADOO4580 Human HPT
12	1241	17.7	1997	5	AAE20278 Human lun
13	1241	17.7	1997	7	ABR57179 Human PTP
14	1241	17.7	1997	7	ADJ70329 Human hea
15	1241	17.7	2002	4	AAW79805 Human pro
16	1230	17.5	1450	7	ABR57182 Human PTP
17	1177.5	16.7	1115	8	ADN12200 Human Sap
18	1140	16.2	1128	8	ABM82538 Human dia
19	1130	16.1	1093	6	ABR43688 Human tyr
20	1127	16.0	1093	6	ABR43689 Human tyr
21	1124.5	16.0	1099	8	ABM82535 Human dia
22	1112	15.8	1102	8	ABE28325 Human KRP
23	1107.5	15.8	1083	8	ABM82537 Human dia
24	1105	15.7	1128	8	ABM82533 Human dia
25	1101	15.7	1531	7	ADBO8753 Novel pro

26	1088	15.5	1112	8	ABM82534 Human dia
27	1079	15.3	1084	4	ABM82536 Human dia
28	1043.5	14.8	1647	4	ABM85428 Drosophi
29	993.5	14.1	579	3	ABH19773 Mouse vas
30	991.5	14.1	1705	5	ABR52348 Protein r
31	969	13.8	1767	4	ABR62726 Drosophi
32	957.5	13.6	1711	5	ABR52349 Protein r
33	954	13.6	1711	2	AAW70506 Osteocyt
34	944	13.4	1711	2	AAW70507 Mutant os
35	924.5	13.2	1447	7	ABR57181 Drosophi
36	889.5	12.7	336	8	ADOO4582 Human HPT
37	879	12.5	1912	8	ADR40183 Human pro
38	878.5	12.5	312	8	ADOO4584 Human HPT
39	878.5	12.5	319	6	ADOO4585 Human HPT
40	864	12.3	2301	6	ABP60058 Human pho
41	855	12.2	1188	2	AAW42991 Amino aci
42	854	12.1	1188	5	ABR52338 Protein r
43	854	12.1	1188	7	ADD89075 TAT779. 1
44	854	12.1	1188	8	ADH17078 Human 207
45	849.5	12.1	1217	7	ADD46195 Rat Proce

ALIGNMENTS

RESULT 1	ADL16193 standard; protein, 1337 AA.
ADL16193	
ADL16193;	
06-MAY-2004 (first entry)	
Human protein tyrosine phosphatase #13.	
cytostatic; immunosuppressive; antiallergic;	
protein tyrosine phosphatase; reversible oxidation;	
inducible signalling pathway; cell proliferation; cancer;	
guest vs. host disease; autoimmune disease; allergy; metabolic disorder;	
cell-cycle abnormality; enzyme.	
Homo sapiens.	
WO2003068984-A2.	
21-AUG-2003.	
13-FEB-2003; 2003WO-EP001446.	
13-FEB-2002; 2002US-0356810P.	
12-FEB-2003; 2003US-00366547.	
(COLD-) COLD SPRING HARBOR LAB.	
(CEPT-) CEPTYR INC.	
Tonks NK, Tzu-Ching M, Cool DE;	
WPI; 2003-712572/67.	
N-PSDB; ADL16192.	
Identifying reversibly oxidized protein tyrosine phosphatase, useful in	
screening for specific modulators, potential agents for treating e.g.	
cancer or autoimmune disease.	
Disclosure; SEQ ID NO 42; 238pp; English.	
The invention relates to a method for identifying a protein tyrosine	
phosphatase (PTP) that is reversibly oxidized in a cell by: (i)	
subjecting a sample, including a cell that contains at least one PTP, to	
conditions that cause reversible oxidation of PTP; (ii) isolating PTP	
aneurobically, in presence of a sulhydryl-reactive agent (IR) that	
irreversibly modifies the thiol group of an invariant Cys in the active	
site of PTP; and (iii) determining, under reducing conditions, the level	

CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.

XX Sequence 1337 AA;

Query Match 100.0%; Score 7030; DB 7; Length 1337;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPAREARLPSPSPGLRWALPLLLLLRLGQILCAGTSPSPIDPPSVATVATGNGITQ 60
 DB 1 MKPAREARLPSPSPGLRWALPLLLLLRLGQILCAGTSPSPIDPPSVATVATGNGITQ 60
 QY 61 ISSIASFKKONGTGTPOVEITNSDESSGANDSLRPEGSGNGTGAQKTPSTGPS 120
 DB 61 ISSIASFKKONGTGTPOVEITNSDESSGANDSLRPEGSGNGTGAQKTPSTGPS 120
 QY 121 PVPDIKAVSISPTNYLLTWKSNDDTAEEKYVVKHMEKITTIVHQPWCNITGLRAT 180
 DB 121 PVPDIKAVSISPTNYLLTWKSNDDTAEEKYVVKHMEKITTIVHQPWCNITGLRAT 180
 QY 181 SYVFSITPGIGNETWGDPRVIVKITEPIPVSDLRVALTGVRAKALSWNGNGTASCRVLL 240
 DB 181 SYVFSITPGIGNETWGDPRVIVKITEPIPVSDLRVALTGVRAKALSWNGNGTASCRVLL 240
 QY 241 BSIGSHEELTQSRLOVNIISDLKPGVQYNINPYLLQSNKTKDPIGTGCGLDASTERSR 300
 DB 241 BSIGSHEELTQSRLOVNIISDLKPGVQYNINPYLLQSNKTKDPIGTGCGLDASTERSR 300
 QY 301 AGSPAPVADBSLVGPVDPSSGQGRDTEVLVGLPEGRVAVATVYSGAANGTEGQPAI 360
 DB 301 AGSPAPVADBSLVGPVDPSSGQGRDTEVLVGLPEGRVAVATVYSGAANGTEGQPAI 360
 QY 361 EFRTAIOVFDTAVNISATSLTLIMKVSNDNESSNYYTKIHVAGETDSNINAVEPRAY 420
 DB 361 EFRTAIOVFDTAVNISATSLTLIMKVSNDNESSNYYTKIHVAGETDSNINAVEPRAY 420
 QY 421 IPGLASSFTFNTTVCPLVGDIEGTGFLQVHTPPVPVSDPFTVAVSTTEIGLAWSSHDAE 480
 DB 421 IPGLASSFTFNTTVCPLVGDIEGTGFLQVHTPPVPVSDPFTVAVSTTEIGLAWSSHDAE 480
 QY 481 SFQMHITQEGAGNSRVEITTNOSIIIGGLFGTKYCFEIVKPGNGTEGASRTVCNRTVP 540
 DB 481 SFQMHITQEGAGNSRVEITTNOSIIIGGLFGTKYCFEIVKPGNGTEGASRTVCNRTVP 540
 QY 541 SAVPDIHVYVYTTTMMLDKSPDGASRYVHLVYESKSGNSHTSTYDKAITLQGLIPGT 600
 DB 541 SAVPDIHVYVYTTTMMLDKSPDGASRYVHLVYESKSGNSHTSTYDKAITLQGLIPGT 600
 QY 601 LYNITISPEVDHVMGDPNSTAQYTRPSVNSINDVSTNTAATLSMONPDDASPTVYCYL 660
 DB 601 LYNITISPEVDHVMGDPNSTAQYTRPSVNSINDVSTNTAATLSMONPDDASPTVYCYL 660
 QY 661 IEKAGNSSNATQVVTIDIGITDATTTELI PGSSSYVEIFPAQVGDGKSLERPKRSFCTDPA 720
 DB 661 IEKAGNSSNATQVVTIDIGITDATTTELI PGSSSYVEIFPAQVGDGKSLERPKRSFCTDPA 720
 QY 721 SMASPDCVVPKPEPLVTKTCPPGANAAGFELVSSGAMNATLJESCSNGTEYRETV 780
 DB 721 SMASPDCVVPKPEPLVTKTCPPGANAAGFELVSSGAMNATLJESCSNGTEYRETV 780
 QY 781 TYLNFSTSYNISITTVSCGKMAAFTRNTCTGTIDPPPDSPNITSVSHNSVYVKSGF 840
 DB 781 TYLNFSTSYNISITTVSCGKMAAFTRNTCTGTIDPPPDSPNITSVSHNSVYVKSGF 840

QY 841 EASHGPIKAVVILITTGAGHPASDVLKTYTDDFKGASDTYTYLLIRTEKGRSQSLSE 900
 DB 841 EASHGPIKAVVILITTGAGHPASDVLKTYTDDFKGASDTYTYLLIRTEKGRSQSLSE 900
 QY 901 VLKTEIDVGNSTLLGYNGKLEPLGSYRACVAGFTNITFHPOKGLIDGAEYSVSRSY 960
 DB 901 VLKTEIDVGNSTLLGYNGKLEPLGSYRACVAGFTNITFHPOKGLIDGAEYSVSRSY 960
 QY 961 SDAVSLPDGPVIGAVFGCIFGALVITVVGGFIFWKRKRKADAKNNVESFOIKPKSKL 1020
 DB 961 SDAVSLPDGPVIGAVFGCIFGALVITVVGGFIFWKRKRKADAKNNVESFOIKPKSKL 1020
 QY 1021 IRVENFEAYFKKQADSNCGFAEYEDLKVGISQPKYAEALBENRKNRYNNVLPYDIS 1080
 DB 1021 IRVENFEAYFKKQADSNCGFAEYEDLKVGISQPKYAEALBENRKNRYNNVLPYDIS 1080
 QY 1081 RVKLSVOTHSIDTDYINANNMFGYHSKKDPIATQGPFLNTLKDFWRWMEKNVVAIIMLT 1140
 DB 1081 RVKLSVOTHSIDTDYINANNMFGYHSKKDPIATQGPFLNTLKDFWRWMEKNVVAIIMLT 1140
 QY 1141 CVEQRTKCEBYWPSKQADYGDITVAMTSEIVLPEWTIRDFYKNIQTSESHPLRQFHF 1200
 DB 1141 CVEQRTKCEBYWPSKQADYGDITVAMTSEIVLPEWTIRDFYKNIQTSESHPLRQFHF 1200
 QY 1201 TSWPDHGVPTDILLINFRILVNDYMKQSPPEPILVHCAGVGRGTGTFIADRLLYQIE 1260
 DB 1201 TSWPDHGVPTDILLINFRILVNDYMKQSPPEPILVHCAGVGRGTGTFIADRLLYQIE 1260
 QY 1261 NENTVDYGIYDLMRMRPLMVGCTEDQYVFLNCCVLDIVSOKDSKYDLIYONTTAMTIY 1320
 DB 1261 NENTVDYGIYDLMRMRPLMVGCTEDQYVFLNCCVLDIVSOKDSKYDLIYONTTAMTIY 1320
 QY 1321 ENLAPVTTFGKNGYIA 1337
 DB 1321 ENLAPVTTFGKNGYIA 1337

RESULT 2

ID ADP74603 standard; protein; 1337 AA.

AC ADP74603;

DT 26-AUG-2004 (first entry)

XX Amino acid sequence of human DEP-1.

KW human; density enhanced phosphatase-1; DEP-1; DEP-1 complex;

KW p120 catenin; adaptor protein; Gab 1; hepatocyte growth factor receptor;

KW HGF receptor; scatter factor receptor; SF receptor; Met; plakoglobin;

KW beta-catenin; signal transduction; cell growth; cell proliferation;

KW cell cycle regulation; contact inhibition; cellular differentiation;

OS Homo sapiens.

PN WO2004048549-A2.

PD 10-JUN-2004.

PF 26-NOV-2003; 2003WO-US038089.

PR 26-NOV-2002; 2002US-0429746P.

PA (COLD-) COLD SPRING HARBOR LAB.

PI Palaka-Hambliin HL, Tonks NK;

DR WPI; 2004-450367/42.

DR N-FSDB; ADP74602.

PT New isolated complex comprises Density Enhanced Phosphatase-1 (DEP-1)

PT polypeptide, useful for manipulating biological signal transduction
 PT pathways, or determining additional molecular components of the pathways.
 XX
 PS Claim 2; Page 95-97; 130pp; English.

CC The present sequence represents a human density enhanced phosphatase-1
 CC (DEP-1) polypeptide. The specification describes DEP-1 complexes,
 CC comprising DEP-1 and DEP-1 substrates. DEP-1 substrate polypeptides that
 CC interact specifically with the substrate-trapping mutant form of DEP-1
 CC are isolated from human breast tumour cell lines. These polypeptides
 CC include the functional component of p120 catenin, the adaptor protein Gab
 CC 1, the hepatocyte growth factor (HGF)/scatter factor (SF) receptor Met, a
 CC plakoglobin polypeptide, and a beta-catenin polypeptide. The DEP-1
 CC complexes are useful for manipulating biological signal transduction
 CC pathways, including defining therapeutic targets, or determining
 CC additional molecular components of such pathways. Agents which modulate
 CC the complexes are useful for therapeutic interventions which influence
 CC biological processes, e.g. cell growth or proliferation including cell
 CC cycle regulation and contact inhibition of cell growth, cellular
 CC differentiation including altered cellular morphogenesis or motility or
 CC other cellular activities characterized by alterations in cytoskeletal
 CC organization and/or cellular gene expression, or cell survival including
 CC cellular responses to apoptotic stimuli.

CC
 XX
 SQ Sequence 1337 AA;

Query Match 100.0%; Score 7030; DB 8; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPARARARLPSPGRLMALPLLLLLRLGQILCAGTSPSPIDPPSVATVATGNGITQ 60
 DB 1 MKPARARARLPSPGRLMALPLLLLLRLGQILCAGTSPSPIDPPSVATVATGNGITQ 60
 QY 61 ISSAESFHKONGTGTPOVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSTPS 120
 DB 61 ISSAESFHKONGTGTPOVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSTPS 120
 QY 121 PVPIKAVISPTNVILTWKNDTRAASKYKVKHKNENKTIIVVHQPMCNITGLRAT 180
 DB 121 PVPIKAVISPTNVILTWKNDTRAASKYKVKHKNENKTIIVVHQPMCNITGLRAT 180
 QY 121 PVPIKAVISPTNVILTWKNDTRAASKYKVKHKNENKTIIVVHQPMCNITGLRAT 180
 DB 121 PVPIKAVISPTNVILTWKNDTRAASKYKVKHKNENKTIIVVHQPMCNITGLRAT 180
 QY 181 SYVSIPTGIGNETWGPDRIVKITEPIVSDLRVALTGVRKAALSMNGNGTASCRVL 240
 DB 181 SYVSIPTGIGNETWGPDRIVKITEPIVSDLRVALTGVRKAALSMNGNGTASCRVL 240
 QY 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLLQSNKTKGDLPGEGGLDASNTESR 300
 DB 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLLQSNKTKGDLPGEGGLDASNTESR 300
 QY 301 AGSPTAPVHDESLVGPVDPSSGQSRDTEVLVGLPESTRNATVYSGAANGTEGQPAI 360
 DB 301 AGSPTAPVHDESLVGPVDPSSGQSRDTEVLVGLPESTRNATVYSGAANGTEGQPAI 360
 QY 361 EFRFNALQVFPVTAVNISATSLTLIMKYSDNESSNNTYKLVHAGETSSMLNVSERAV 420
 DB 361 EFRFNALQVFPVTAVNISATSLTLIMKYSDNESSNNTYKLVHAGETSSMLNVSERAV 420
 QY 421 IPGRASSTFNITVCPVLGDIETPGFLQVATPPVPSDFRVTVSTTEIGLAWSHDAE 480
 DB 421 IPGRASSTFNITVCPVLGDIETPGFLQVATPPVPSDFRVTVSTTEIGLAWSHDAE 480
 QY 481 SFQWHTIOEGAGNSRVEITTNQSIITIGLFPETKCCFEIVKSGNGTEGARTVCNRVTP 540
 DB 481 SFQWHTIOEGAGNSRVEITTNQSIITIGLFPETKCCFEIVKSGNGTEGARTVCNRVTP 540
 QY 541 SAVFDIHVVYVYTTTMMTLDKSPDGASEYVHLVIESGHGSHNTSYKATITLQGLIPGT 600
 DB 541 SAVFDIHVVYVYTTTMMTLDKSPDGASEYVHLVIESGHGSHNTSYKATITLQGLIPGT 600
 QY 601 LYNITISPEVDHWGDPNSTAQYTRPSNVSNIDVSTNTAAATLSWQNFDDASPTYSYCLL 660
 DB 601 LYNITISPEVDHWGDPNSTAQYTRPSNVSNIDVSTNTAAATLSWQNFDDASPTYSYCLL 660

QY 661 IEKAGNSNATQVYTDIGITDATVTELLPGSSYVEIFAQVGDGIKSLERPKRSFCTDPA 720
 DB 661 IEKAGNSNATQVYTDIGITDATVTELLPGSSYVEIFAQVGDGIKSLERPKRSFCTDPA 720
 QY 721 SMASFDCEVVPKEBALVTKTCCPGANAGFELVSSGAMNNATHLSCSSENGTEYRTVEV 780
 DB 721 SMASFDCEVVPKEBALVTKTCCPGANAGFELVSSGAMNNATHLSCSSENGTEYRTVEV 780
 QY 781 TYLNFSTSYNISTITVSCGKMAATRTCTTGITDPPPPGSPNITSVSHSVYVKSGF 840
 DB 781 TYLNFSTSYNISTITVSCGKMAATRTCTTGITDPPPPGSPNITSVSHSVYVKSGF 840
 QY 841 EASHGPVKAAYVILTTGAGHPSADVLTKYTDDPKKASDPTVYVYLIRTEBKGSQSLSE 900
 DB 841 EASHGPVKAAYVILTTGAGHPSADVLTKYTDDPKKASDPTVYVYLIRTEBKGSQSLSE 900
 QY 901 VLKYEIDVGNESSTLGYNGKLEBLSGYRACVAGFTNITPHQNGKLIIDGASVVSFRY 960
 DB 901 VLKYEIDVGNESSTLGYNGKLEBLSGYRACVAGFTNITPHQNGKLIIDGASVVSFRY 960
 QY 961 SDAVSLQDDPQVITGAVFGCIPGALVITVGGFIFWKKRRKADAKNEVSFQIKPKSKL 1020
 DB 961 SDAVSLQDDPQVITGAVFGCIPGALVITVGGFIFWKKRRKADAKNEVSFQIKPKSKL 1020
 QY 1021 IRVENFEAYFKQOADSNCGFAEYEDLKVGISQPKYAAELANRGNRYNNVLPYDIS 1080
 DB 1021 IRVENFEAYFKQOADSNCGFAEYEDLKVGISQPKYAAELANRGNRYNNVLPYDIS 1080
 QY 1081 RVKLSVQTHSTDDYINANNMFGVHKKDPIATQGPLPNTLKDFFRMWKKNNVAILMLTK 1140
 DB 1081 RVKLSVQTHSTDDYINANNMFGVHKKDPIATQGPLPNTLKDFFRMWKKNNVAILMLTK 1140
 QY 1141 CVEGRTKCEBYWWSKQADYDGTIVANTSTIVUPENTIRDPYTKNIQTSSSHLRQPHF 1200
 DB 1141 CVEGRTKCEBYWWSKQADYDGTIVANTSTIVUPENTIRDPYTKNIQTSSSHLRQPHF 1200
 QY 1201 TSWPDHGVPTDLDLINFRIYVRDYMKOSPESPILVHCSAGVGTGFIAIDRLIYOIE 1260
 DB 1201 TSWPDHGVPTDLDLINFRIYVRDYMKOSPESPILVHCSAGVGTGFIAIDRLIYOIE 1260
 QY 1261 NENTVDVYGIYDRLMRPLMVQTEDOYVFLNQCVLDIVRSQKSKVDLIYQNTTAMTIV 1320
 DB 1261 NENTVDVYGIYDRLMRPLMVQTEDOYVFLNQCVLDIVRSQKSKVDLIYQNTTAMTIV 1320
 QY 1321 ENLAPVTTFGKTNGYIA 1337
 DB 1321 ENLAPVTTFGKTNGYIA 1337

RESULT 3
 ADL16195
 ID ADL16195 standard; protein; 1337 AA.
 XX
 AC ADL16195;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human protein tyrosine phosphatase #14.
 XX
 KW cytosolic; immunosuppressive; anti-allergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signalling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 RN WO2003068984-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-EP001446.

KM Density enhanced Type III receptor-like protein tyrosine phosphatase;
 KM hudep-1.
 XX
 OS Homo sapiens.
 XX
 FN MO9530008-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 03-MAY-1995; 95MO-US005512.
 XX
 PR 03-MAY-1994; 94US-00237940.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Tonks NK, Oestman A;
 XX
 DR WPI; 1995-393079/50.
 XX
 DR N-PSDB; AAT06027.
 XX
 PT New density enhanced protein tyrosine phosphatase - used to develop
 PT prods. to modify transcription, translation and activity of tyrosine
 PT phosphatase(s).
 PS
 PS Claim 4; Page 34-38; 51pp; English.
 XX
 CC A cDNA clone was obtd. (see AAT06027) from a HeLa cell cDNA library that
 CC encoded a novel density-enhanced Type III receptor-like FTR, designated
 CC hudep-1 (AAR5203). hudep-1 is useful for the study of ptps and for the
 CC development of therapeutic or prophylactic cpds. e.g. for prevention of
 CC abnormal or malignant cell growth
 XX
 SQ Sequence 1337 AA.

Query Match 97.1%; Score 6824; DB 2; Length 1337;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;

QY 1 MKPAAERARLPBRPGLRMALPLLLLRLLGQILCAGTSPSPIDPSVATVATGNGTQ 60
 DB 1 MKPAAERARLPBRPGLRMALPLLLLRLLGQILCAGTSPSPIDPSVATVATGNGTQ 60
 QY 61 ISSAESFHKONGTGPQVETNTSEDESGANDSLRTEQSGNGTDGASQKTPSSGPS 120
 DB 61 ISSAESFHKONGTGPQVETNTSEDESGANDSLRTEQSGNGTDGASQKTPSSGPS 120
 QY 121 PVFDIKAVSISPTNVLTKMSNDTAASEKYVVKHKMENEKTIIVVHQPMCNITGLRPAT 180
 DB 121 PVFDIKAVSISPTNVLTKMSNDTAASEKYVVKHKMENEKTIIVVHQPMCNITGLRPAT 180
 QY 181 SYVESITPGIGNETWGDPRVTKVTEPIVPSDLRYALTGVRKALSMNGNGTASCRVLL 240
 DB 181 SYVESITPGIGNETWGDPRVTKVTEPIVPSDLRYALTGVRKALSMNGNGTASCRVLL 240
 QY 241 ESTGSHEELNODSLQVNIIDLKPGVOYNINPYLLQSKTKGDPGLTEGGLDASTEKSR 300
 DB 241 ESTGSHEELNODSLQVNIIDLKPGVOYNINPYLLQSKTKGDPGLTEGGLDASTEKSR 300
 QY 301 AGSFAPVHDESLVGPVDPSSGQSRDTEVLVLGLEPSTRYNATVYSGAANGTEGQPAI 360
 DB 301 AGSFAPVHDESLVGPVDPSSGQSRDTEVLVLGLEPSTRYNATVYSGAANGTEGQPAI 360
 QY 361 EFRFNAIOVFNVTAVNISATSLTLIMKYSDNSSSNNTYKTHVAGETSSNLNVEPAV 420
 DB 361 EFRFNAIOVFNVTAVNISATSLTLIMKYSDNSSSNNTYKTHVAGETSSNLNVEPAV 420
 QY 421 IPRGRSSTFNITVCPVLGDIETGPGFLOVHTPPVPSDFRTVYVSTTEIGLANSHPAB 480
 DB 421 IPRGRSSTFNITVCPVLGDIETGPGFLOVHTPPVPSDFRTVYVSTTEIGLANSHPAB 480
 QY 481 SFQNHITDGGAGNSRVEITTNQSIIGGLPFGTKYCFEIVKPGNGTEGASRTVCNRTVP 540
 DB 481 SFQNHITDGGAGNSRVEITTNQSIIGGLPFGTKYCFEIVKPGNGTEGASRTVCNRTVP 540

QY 541 SAVFDIHVVYTTTMMMLDMKSPDGASEYVYHLVIESKSGSNHTSTYDKAITLLOGLPGT 600
 DB 541 SAVFDIHVVYTTTMMMLDMKSPDGASEYVYHLVIESKSGSNHTSTYDKAITLLOGLPGT 600
 QY 601 LYNITISPEVDHVGNDNSTAQYTRPSNVSNIDVSTNTTAATLSWONFDDASPTYSYCLL 660
 DB 601 LYNITISPEVDHVGNDNSTAQYTRPSNVSNIDVSTNTTAATLSWONFDDASPTYSYCLL 660
 QY 661 IEKAGNSNATQVYTDGITDATYTELIPGSSYVVELPAOVGDGIKLEPERKSPCTDPA 720
 DB 661 IEKAGNSNATQVYTDGITDATYTELIPGSSYVVELPAOVGDGIKLEPERKSPCTDPA 720
 QY 721 SMASFDCVVPKEPALVLKMTCPPGANAGFELVSSGAMNNAATLIESCSSNGTEYRTREV 780
 DB 721 SMASFDCVVPKEPALVLKMTCPPGANAGFELVSSGAMNNAATLIESCSSNGTEYRTREV 780
 QY 781 TYLNFSTSYNISITTVSGKMAAPTRNTCTGTIDPPPDGSPNITSVSHNSVVKSGCF 840
 DB 781 TYLNFSTSYNISITTVSGKMAAPTRNTCTGTIDPPPDGSPNITSVSHNSVVKSGCF 840
 QY 841 EASHGPIKAVAVILITGBAGHPSADVLYKTYDDPKKASDPTVYVYLIRTEKGRSQSLSE 900
 DB 841 EASHGPIKAVAVILITGBAGHPSADVLYKTYDDPKKASDPTVYVYLIRTEKGRSQSLSE 900
 QY 901 VLKYEIDVGNSESTLGYNGKLEPLGSYRACVAGFTNITFHPONKGLIDGAEYSVSFSRY 960
 DB 901 VLKYEIDVGNSESTLGYNGKLEPLGSYRACVAGFTNITFHPONKGLIDGAEYSVSFSRY 960
 QY 961 SDAVSLPDQPGVICGAVFGCIFGALVITVVGFI FWRKKRDAKONNEVSFSQIKPKSKL 1020
 DB 961 SDAVSLPDQPGVICGAVFGCIFGALVITVVGFI FWRKKRDAKONNEVSFSQIKPKSKL 1020
 QY 1021 IRVENFEAYFKKQADNSNCGFAEYEDLKLVGISQPKYAAALANRGNRRNNLTPYIS 1080
 DB 1021 IRVENFEAYFKKQADNSNCGFAEYEDLKLVGISQPKYAAALANRGNRRNNLTPYIS 1080
 QY 1081 RVKLSVOTHSITDDIYNNANPMGYHSKKDPIATQGPLPTLKDPMRWMEKVVVAILMLTK 1140
 DB 1081 RVKLSVOTHSITDDIYNNANPMGYHSKKDPIATQGPLPTLKDPMRWMEKVVVAILMLTK 1140
 QY 1141 CVEQGRTKCEBYWPSKQADYDGIITVAMTSEIVLPEWTRIDFTYKNIQTSSHPLRQHF 1200
 DB 1141 CVEQGRTKCEBYWPSKQADYDGIITVAMTSEIVLPEWTRIDFTYKNIQTSSHPLRQHF 1200
 QY 1201 TSWPDHGVPDPTDLLINFRYLVRDYMKQSPBSPILVHCSAGVGRGTGFIADRLIYQIE 1260
 DB 1201 TSWPDHGVPDPTDLLINFRYLVRDYMKQSPBSPILVHCSAGVGRGTGFIADRLIYQIE 1260
 QY 1261 NENTVDVYGIYDILRMHRPLMVOTEDQVFLNQCVLDIIVRSQSKVDLLIYQNTTAMTIY 1320
 DB 1261 NENTVDVYGIYDILRMHRPLMVOTEDQVFLNQCVLDIIVRSQSKVDLLIYQNTTAMTIY 1320
 QY 1321 ENLAPVTTFGKTNGYIA 1337
 DB 1321 ENLAPVTTFGKTNGYIA 1337

RESULT 5
 ADL16198
 ID ADL16198 standard; protein; 1238 AA.
 AC ADL16198;
 DT 06-MAY-2004 (first entry)
 XX
 DE Mouse protein tyrosine phosphatase #4.
 XX
 XX cytosolic; immunosuppressive; antiallergic;
 KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KM inducible signalling pathway; cell proliferation; cancer;
 KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KM cell-cycle abnormality; enzyme.

ID	ADL16200	standard; protein; 1216 AA.
AC	ADL16200;	
XX		
DT	06-MAY-2004	(first entry)
XX		
DE	Rat protein tyrosine phosphatase #4.	
XX		
KW	cytostatic; immunosuppressive; antiallergic;	
KW	protein tyrosine phosphatase; reversible oxidation; dephosphorylation;	
KW	inducible signalling pathway; cell proliferation; cancer;	
KW	guest vs. host disease; autoimmune disease; allergy; metabolic disorder;	
KW	cell-cycle abnormality; enzyme.	
XX		
OS	Rattus norvegicus.	
XX		
PN	MO2003068984-A2.	
XX		
PD	21-AUG-2003.	
XX		
PF	13-FEB-2003; 2003MO-EP001446.	
XX		
PR	13-FEB-2002; 2002US-0356810P.	
XX		
PR	12-FEB-2003; 2003US-00366547.	
XX		
PA	(COLD-) COLD SPRING HARBOR LAB.	
XX		
PI	(CEPT-) CEPTYR INC.	
XX		
PI	Tonks NK, Tzu-Ching M, Cool DE;	
XX		
DR	WPI; 2003-712572/67.	
XX		
DR	N-PSDB; ADL16199.	
XX		
PT	Identifying reversibly oxidized protein tyrosine phosphatase, useful in	
XX	screening for specific modulators, potential agents for treating e.g.	
XX	cancer or autoimmune disease.	
XX		
XX	Disclosure; SEQ ID NO 49; 238bp; English.	
XX		
PS	The invention relates to a method for identifying a protein tyrosine	
XX	phosphatase (PTP) that is reversibly oxidized in a cell by: (i)	
CC	subjecting a sample, including a cell that contains at least one PTP, to	
CC	conditions that cause reversible oxidation of PTP; (ii) isolating PTP	
CC	anaerobically, in presence of a sulphydryl-reactive agent (ii) that	
CC	irreversibly modifies the thiol group of an invariant Cys in the active	
CC	site of PTP; and (iii) determining, under reducing conditions, the level	
CC	of dephosphorylation, caused by PTP, of a labelled substrate (iii), where	
CC	dephosphorylation indicates that an active PTP is present.. No details	
CC	of tests for these activities are given. The method is used to identify	
CC	reversibly oxidized PTP, also to identify agents that: (a) reversibly	
CC	modify such PTP; or (b) alter inducible signalling pathways in which PTP	
CC	are involved. These agents are potentially useful, in human or veterinary	
CC	medicine, for treating abnormal cell proliferation or growth (cancer);	
CC	guest vs. host disease; autoimmune diseases; allergy or other	
CC	immunosuppressed states; metabolic disorders and cell-cycle	
CC	abnormalities. This sequence represents one of the PTP enzyme of the	
CC	invention.	
XX		
XX		
SO	Sequence 1216 AA;	
XX		
Qy	Query Match	64.0%; Score 4499.5; DB 7; Length 1216;
XX	Best Local Similarity	67.1%; Pred. No. 5.2e-292;
XX	Matches 900; Conservative 106; Mismatches 202; Indels 131; Gaps 10;	
Db	1 MKPARBARLPRSGRLWMLPLLLLRGLGACGPPSPIPPSPVATVATGNGITG 60	
XX		
XX	1 MKPARRRRTTPRSGLRWMLPLLLLRKGGVCTG----- 37	
Qy	61 ISSTAESHKONGTGPQVETVTSDEGSSGANDLRTPEQSGNGTDGASQKTPSGTGS 120	
XX		
Db	38 -----AAPS 41	
Qy	121 VPFDIKAVISPTNVLITWKSNDTAASEYKVVAKHMEKNTITVHOPMCNITGLRPAT 180	

[illegible]

Db 1075 RQFHTSWPDHGVDPDTDLLINFRYLVRDYMKQIPPESPILVHCASGVRGTGFIADRL 1134
 QY 1256 IYGIENENTVDYGIYVDLRRHRLPMVQTEQYVFLNOCYLDIVRSQKSKVDLIYQNTT 1315
 Db 1135 IYGIENENTVDYGIYVDLRRHRLPMVQTEQYVFLNOCYLDIIRAKOSKVDLIYQNTT 1194
 QY 1316 AMTIYENLAPVTTEGKTNGYIA 1337
 Db 1195 AMTIYENLERSVWFGKANGYIA 1216

RESULT 7
 ADP74604
 ID ADP74604 standard; peptide; 341 AA.
 XX
 AC ADP74604;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Amino acid sequence of a human DEP-1 fragment.
 XX
 KW human; density enhanced phosphatase-1; DEP-1; DEP-1 complex;
 KW p120 catenin; adaptor protein; Gab 1; hepatocyte growth factor receptor;
 KW HGF receptor; scatter factor receptor; SF receptor; Met; plakoglobin;
 KW beta-catenin; signal transduction; cell growth; cell proliferation;
 KW cell cycle regulation; contact inhibition; cellular differentiation;
 KW cellular morphogenesis; cellular motility; cytoskeleton.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048549-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038089.
 XX
 PR 26-NOV-2002; 2002US-0429746P.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Palaka-Hamblin HL, Tonks NK;
 XX
 DR WPI; 2004-450367/42.
 XX
 PT New isolated complex comprises Density Enhanced Phosphatase-1 (DEP-1)
 PT polypeptide, useful for manipulating biological signal transduction
 PT pathways, or determining additional molecular components of the pathways.
 XX
 PS Claim 2; Page 98; 130pp; English.

The present sequence represents a human density enhanced phosphatase-1 (DEP-1) fragment, comprising residues 997-1337 of ADP74603. The specification describes DEP-1 complexes, comprising DEP-1 and DEP-1 substrates. DEP-1 substrate polypeptides that interact specifically with the substrate-trapping mutant form of DEP-1 are isolated from human breast tumour cell lines. These polypeptides include the functional component of p120 catenin, the adaptor protein Gab 1, the hepatocyte growth factor (HGF)/scatter factor (SF) receptor Met, a plakoglobin polypeptide, and a beta-catenin polypeptide. The DEP-1 complexes are useful for manipulating biological signal transduction pathways, including defining therapeutic targets, or determining additional molecular components of such pathways. Agents which modulate the complexes are useful for therapeutic interventions which influence biological processes, e.g. cell growth or proliferation including cell cycle regulation and contact inhibition of cell growth, cellular differentiation including altered cellular morphogenesis or motility or other cellular activities characterized by alterations in cytoskeletal organization and/or cellular gene expression, or cell survival including cellular responses to apoptotic stimuli.

Sequence 341 AA;

Query Match 25.8%; Score 1811; DB 8; Length 341;

Best Local Similarity 100.0%; Pred. No. 1e-112;
 Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 RKRKDAKNNEVSFSQIKPKKSKLIRVENFEAFYFKQAOASNGFAEYEDLKLVG:SQP 1056
 Db 1 RKRKDAKNNEVSFSQIKPKKSKLIRVENFEAFYFKQAOASNGFAEYEDLKLVG:SQP 60
 QY 1057 KYAAELAMNKGKRNRYNVLPRDISRVKLSVQTHSTDDYINANNYPGYHKKDDFIATQGPL 1116
 Db 61 KYAAELAMNKGKRNRYNVLPRDISRVKLSVQTHSTDDYINANNYPGYHKKDDFIATQGPL 120
 QY 1117 PNTLKDFRWVMEQNVYAIIMLTCKVCGRPKCEYWPSPKQAOYGGITVAMSEIYLPE 1176
 Db 121 PNTLKDFRWVMEQNVYAIIMLTCKVCGRPKCEYWPSPKQAOYGGITVAMSEIYLPE 180
 QY 1177 WTIRDFTVKNIQTSSEHPRLQFHTSWPDHGVDPDTDLLINFRYLVRDYMKQSPPEPSPIL 1236
 Db 181 WTIRDFTVKNIQTSSEHPRLQFHTSWPDHGVDPDTDLLINFRYLVRDYMKQSPPEPSPIL 240
 QY 1237 VHCSAGVGRGTGFIADRLIYGIENENTVDYGIYVDLRRHRLPMVQTEQYVFLNOCYL 1296
 Db 241 VHCSAGVGRGTGFIADRLIYGIENENTVDYGIYVDLRRHRLPMVQTEQYVFLNOCYL 300
 QY 1297 DIVRSQKSKVDLIYQNTAMTIYENLAPVTTEGKTNGYIA 1337
 Db 301 DIVRSQKSKVDLIYQNTAMTIYENLAPVTTEGKTNGYIA 341

RESULT 8
 AAO24268
 ID AAO24268 standard; protein; 1998 AA.
 XX
 AC AAO24268;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Murine vascular endothelial-protein tyrosine phosphatase.
 XX
 KW Vascular endothelial protein-tyrosine phosphatase; VE-PTP; mouse; human;
 KW gene therapy; cytosstatic; VE-cadherin; vascular endothelial-cadherin.
 XX
 OS Mus sp.
 XX
 PN WO2003084565-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 08-APR-2003; 2003WO-EP003645.
 XX
 PR 08-APR-2002; 2002EP-00007837.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Nawroth R, Deutsch U, Vestweber D, Shima DT, Golding M;
 XX
 DR WPI; 2003-804251/75.
 XX
 PT Use of the polypeptide comprising vascular endothelial-protein tyrosine
 PT phosphatase (VE-PTP) or the nucleic acid encoding the polypeptide for the
 PT manufacture of an agent for monitoring or modulating VE-cadherin mediated
 PT disorders.
 XX
 PS Example; Fig 2; 0pp; English.

The present invention relates to a polypeptide comprising vascular endothelial-protein tyrosine phosphatase (VE-PTP) or its active fragment or effector, or the nucleic acid encoding the polypeptide or its effector, for use in the manufacture of an agent for monitoring or modulating VE-cadherin mediated processes or disorders. The polypeptide comprising vascular endothelial-protein tyrosine phosphatase (VE-PTP) or its active fragment or effector, or the nucleic acid encoding the polypeptide or its effector, is useful for the manufacture of an agent for monitoring or modulating VE-cadherin mediated processes or disorders,

CC e.g., cancer. The present sequence is a protein shown in the
 CC exemplification of the invention
 XX
 SQ Sequence 1998 AA:

Query Match 17.9%; Score 1259.5; DB 7; Length 1998;
 Best Local Similarity 28.8%; Pred. No. 1.5e-74;
 Matches 378; Conservative 216; Mismatches 500; Indels 217; Gaps 45;

QY 104 NGIDGASQKTPSSGSPSPVPDIKAVSISPTNVLITWMSNDTAASEYKVKVGHKNEKTI 163
 DB 805 SGQYAEBOEGRTIPPEVVKDLTLINSTEDLHVTWNRANDVOYE--VOLLFNDMKVF 862
 QY 164 TVVHQPCNITGLRPAITSYF-SITPG-----IGNETWGDPR--VIKITEPIVPSDLR 214
 DB 863 PHIL-----VTAITEYKTAIPGRHKILVLTISGDVQSAFIEGLVPESTVKNIH 915
 QY 215 VALTVR-KAALSWNSNGTASCRVLLSISGHEELTODSRLQVNIISDLKPGVQYINPY 273
 DB 916 ISANGATDRLMVTWSPGG-----DVDSY 939
 QY 274 LLSGNTKKGDLTGEGGLDASNTSRASGPTAPVHDESLVGPDPSSGQOSRDTVLV 333
 DB 940 VVSAFR-----ODEKVDSCQIPIKH-----ASEHTFH 965
 QY 334 GLEPRTYNAITVVSQAANGTEGQPAIEFRINAIOVDYTAVN--ISATSLTIWKVSDNE 392
 DB 966 RLEAGAKRTAIVS-VGSLSRNQIDALG-QTVPASQGVAAVYSSLSLVSQKALGV 1023
 QY 393 SSSNYTKIHVAGETDSSNLNVSEPPRA-----VIPGLASSTFYNTVCPVLGDIET 444
 DB 1024 AE---RDILLINENGLLSVSESPATARQHKFEDLTPGKK-----YKQILTVGGGLFSK 1076
 QY 445 PGFLQVHTPPVVSDFRYTVSTTEIGLASHDAESFOHMI---TOEGANSVEI-TT 500
 DB 1077 ESQAGRTVPAVYVNLRLITENSSRYLSFGWTASGELISWNIPLYNPDRLOEBAQVDPL 1136
 QY 501 NQSIIGLPGFTYCEBIYKPGNGTEGASRTVCNTRVPSADIVHVVYTTRE-WMLD 559
 DB 1137 VQSEFQNLQGRMYKAVIYVH--SGELSNESFIFGRVQPAVYVNLKSHNTDLSLFS 1194
 QY 560 WKSPDGASEVYVHLVIESKGSNHTSTYDKAIT--LOGLIIPG--TLYNITISPEVDH 613
 DB 1195 WSPASGPDF-YELLVNPNGTKENMKKQVTEMREGVLPGKRYLTVYVTHSGDLSNK 1253
 QY 614 WQDPNSTAQOTRPSNVSNIDYSTNTTAATL---SKQNFEDAS---PTSYCLILKAG 665
 DB 1254 VTGEGRTAP-SPELSLFAVDVANTSLAITWKGPPDWTIDYDFELQWFGDALITFNPYS 1312
 QY 666 NSSNATQVVDIGITDATTVELIPGSSYTVEIFAIVGDIKSL-EPRGKSCPTDPASMAS 724
 DB 1313 RKSQSG-----RIVYGLHPRSTYQFSVKTSGDMSWTSKPISGSRYTPDKIQN 1361
 QY 725 FDCEVVEKEPALVLKWTCPGANAGFELEVSAGMANNATHLSCSENGETRYTEVTYIN 784
 DB 1362 LHCR-PQNSTALIASWIPBDFDGYSE-----CRKMDTGEIESRKLGEKSLIN 1412
 QY 785 F-----STSYNISITTVSCGMAAPTNCTTGTIDPPPDGSPNI-----TSVSHNSV 833
 DB 1413 IMMLVPHKRYLVSIKIVQSAGWTSSEVEDSTITMIDRPPQ--PHIRVNEKDVLSKSSI 1470
 QY 834 K--VKPSGFASHGPIKAVANIILTTG-----EAGHPSADVLYKTYDDPKKASDPYV 883
 DB 1471 NPTVNCWSPDSTNAVKYFAVVVREADSMDELKPEQGHPLPSYLEIRNASIRYQYNY- 1529
 QY 884 TYLIRTEKGRSQGLSEVLKYEIDVNESTLTG-----YNGKLEPLGSYRACVAG 934
 DB 1530 -PASKCAESPSSSSK-----FNIKLGAEMDSLGGKCPDSQOKFCDDGLKPTAIRISIRA 1584
 QY 935 PTNITPHQKGLIDGASVYSFSRYSDAVSLPDDP-GVICGAVFGCIFALVIYVYG 992
 DB 1585 FTQLF-----DEDLKEFTKPLYSDFPFSWPIITTESEPLFVGIEVSAGIFLIGMLVALVAF 1640

QY 993 FIFWRK--KSKDANKNEVSESQIKP-----KSKLIRVENFEAYFKKQOADS 1037
 DB 1641 FICQKASHSRERPSARLSIRDRPLSVHLNLGQKGRKISCPKINQFESHPKLOADS 1700
 QY 1038 NCGFAEYEDIKLVGISQPKYAAELANRGNRYNNVLPYDISVKLS-VQTHSTDYIN 1096
 DB 1701 NYLLSKSEYEDIKDVGRSQCDIALPENRGNRYNNILPYDASHVKLSNVDDDCSDYIN 1760
 QY 1097 ANWAGYHKKDPIATOGPLPNTLKDFWRVWYKENVVAIIMLTVCVEQGRTKCEYWPSPK 1156
 DB 1761 ASYIPGNVFRREYIATOGPLGTYDDPKWAMBOYVNIIVVTOCVBERKRYKCDHYEPAD 1820
 QY 1157 Q-AQYGDITVAWNTSEIYLPWTIRDFTVAKNIQTSSEHPL-ROPHFTSWPDHGVPTDIL 1214
 DB 1821 QDPLVYGDILIQWSESVLPWTIRREFKICSEBQDLHRLIRHHTYVWPDHGVPTTQS 1880
 QY 1215 LINFYLVRYDMKSPSPSPILVHCSAGVGTGTFIADRLIYQIENENTVYGYIYDL 1274
 DB 1881 LIQFRTVRDYINRSPGAPTVVHCSAGVGTGTFVALDRILQQLDSKSDYIGAVHDL 1940
 QY 1275 RMHRPLAVQTEQVVFVFNQCVLDIVRSQKSKVDLIYQNTAMTYENLAP 1325
 DB 1941 RLHRVHWQTEQVYVLIHQCVRDYLAKKLRN---BOENPLFPIYENVP 1987
 RESULT 9
 ID AAB19774 standard; protein; 1997 AA.
 XX AAB19774;
 DT 19-FEB-2001 (first entry)
 XX
 DE Human protein tyrosine phosphatase HPTP-beta.
 XX
 KW Protein tyrosine phosphatase; HPTP-beta; human; Tie-2;
 KW receptor-type tyrosine kinase; antiangiogenic; antitumor;
 KW antimetastatic; tumour; metastasis; angiogenesis; therapy.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1622..1641
 FT /note= "transmembrane domain"
 FT Domain 1722..1967
 FT /note= "catalytic domain"
 XX
 PN EP1046715-A1.
 XX
 PD 25-OCT-2000.
 XX
 PF 23-APR-1999; 99EP-00108074.
 XX
 PR 23-APR-1999; 99EP-00108074.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Fachinger G, Risa B, Deutsch U;
 DR MPI; 2000-648932/63.
 DR N-PSDB; AAA88866.
 XX
 PT Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g. for
 PT regulating tumor growth, using vascular-endothelial protein tyrosine
 PT phosphatase.
 PS
 SS Disclosure; Page 21-27; 60pp; English.
 CC The present sequence is that of human protein tyrosine phosphatase HPTP-
 CC beta, a member of subclass III receptor type PTPs, bearing fibronectin
 CC type III-like repeats in the extracellular domain and a single catalytic
 CC domain in the cytoplasmic tail. HPTP-beta is a vascular-endothelial
 CC protein tyrosine phosphatase (VE-PTP) that specifically interacts with

XX MPI; 2001-476283/51.
 DR N-PSDB; AAK51954.
 XX
 PT Nucleic acid encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.
 PS Claim 20; Page 3761-3764; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 encoded polypeptides (AAK478323-AAK80302) that exhibit activity elating to
 cytokine, cell proliferation or cell differentiation or which may induce
 production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 1997 AA;
 Query Match 17.7%; Score 1242; DB 4; Length 1997;
 Best Local Similarity 29.6%; Pred. No. 2.2e-73;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
 QY 123 FDIKAVSISPTNVLITKSNDDTAEEYVVKHNEKEKTTIVHQPWCNITGLRPAITSY 182
 DB 759 FDHVEVITIKNNKNIQTKEIP-----KSENE-----CVFVQVLPGRLY 796
 QY 183 VFSTITPIG-----NETMGDRVIVKITEBPVSDLRVALTGVRKAALSMNGNTASGRV 238
 DB 797 SVVYTTSGGYEANEQ-GNGRTI-----PEPVKDLITLRNSTDIEDLHYWSSANG----- 844
 QY 239 LLESIGSHE--ELQDSRL-----QVNISDLKPGVQ-----NINPYLLSKNT 280
 DB 845 ----DVQYEIQLFNDMKVPFPHLVNTATERYRFTSLTPGKQYKLVLTISGDVQDSAFI 901
 QY 281 KG-----DPLG-----TEGLDASN-----TERSRAPSPAFVHDESL 313
 DB 902 EGFVPSAVKNIHISPGATDSLTVNMTPGGDVDSYVSAFRSQKVDSTIPKH----- 957
 QY 314 VGPVDPSSGQOSRTEVLVGLPEGTRYNATVYQAANGTEGQQAIEFRNALQVEDYT 373
 DB 958 -----VFEHTFHLLEAGBOYQIIMAS--VSGSLKQINIVVGRTPVAPVQGV 1002
 QY 374 AVN-ISATSLTLIKVSDNESSNYTKIHVAGETDSSNLVSEPR-----VIRGL 424
 DB 1003 ADNAVSSYSILVSKQAGAAVAE---RYDILITLNGILLRRTSEBATTQKQKFEDELTPGK 1059
 QY 425 RASSTFNITVCPVLIDEGTPGLQVHTPPVPSDFRTVAVSTTEIGLAWSHDAESFQM 484
 DB 1060 K-----YKIQILTVSGGLFESKAQTEBRIVPAALVDTLRTEKSTHLSFRWASGELSMY 1115
 QY 485 HI---TOEGAGNSVEI--TTNQSIIGGLPFGTYCEIYVKGNGTEGASRTVCNRTVP 540
 DB 1116 NIFLYNPDGNLOERAQVDFLVQSFSPQNLQGRMYKWIYTH--SGELSNESFIFGRVVP 1173
 QY 541 SAVVDIHVVVYVTTTE--WMLDKSPDASBYVYHIVISKHSNHTSYDKAIT---LQGL 596
 DB 1174 ASVSHLGSNKNRNTIDSLTFMNSPASGDPDF--YELILNPNSTKKEKWKDKDLTEWRQGL 1232
 QY 597 IPGTLVNTITSPEDVHWGDPNSTAQYTR-----PSNVSNIDVSTNTTAAVL---SNQN 647
 DB 1233 VPGKRYVLMV---VTHSGDLSNKVTASRTPASPSLSMFPDIAMTSLATIMWKQRPMDTD 1289
 QY 648 FDDASPTV---SYCLLIEKAGNSSNATQVVTDIGITDATTTELLPGSSYTYEIRAQVGDG 704
 DB 1290 YNDFELQWLPKDALTVNPNYNNRKESEGRIVYG-----LRPGRSYQFNVKTVSGDS 1339

QY 705 IKSL-EBGRKSFCTDPASMASFDCEVVPKEBPAVLKWTCPGANAGLEEVSSGAMNNAT 763
 DB 1340 WKTVSKCIFSGSVRTKPKIQNLHCR--PQNSTALACSMWIPDSDDPGYSIE-----CR 1390
 QY 764 HLESCSENGTEYRTTYLNF-----STSYNISITTVSGCKMAAPRINTCTGTTDPP 818
 DB 1391 KMDTQEVFERKLEKEKSLNIMLVPHKRYLVSIKVQASGAMTSEVEDSTTMTIDRPP 1450
 QY 819 PDGSPNI-----TSVSHNSVK--VKFSGFASHGPDKAVAVILTTG-----EAGHP 862
 DB 1451 P--PPHIVNEKDVILKSSINFTVNCSPWSDTNGAVKTFVYVVRADGSELKPEQHP 1508
 QY 863 SADVLKTYDDFKKASDYVYVYLIRTEKGRSQSLSEVLKYEIDVNGESTTLG----- 916
 DB 1509 LPVLEYERHNASIVYQTNV--FASKCAENPNSNKS-----FNIKLAGEMSLGKCDPT 1562
 QY 917 ---YTNKLEPLSGYRACVAGFTNITHPONKGLIDGAEVSVSSR--YSDA-VSLP--- 967
 DB 1563 QQKCDPPLKPHYVYRISIFAFTD-----LFD--EDLKEPTKLYSDTFPSLPTT 1611
 QY 968 -QDPGVICGAVFGCIFGALVY---VTVGFIWREKX---RDAKNNVESFSQIKP----- 1015
 DB 1612 ESEP--LFGAIEGVSAQLFLGMLVAVVALLICQKVSNGRERSARLSTRDRPLSVHL 1669
 QY 1016 -----KSKLIRVENFEAYFPKKQADNSNGFAEYEDLKLVGISQPKYAAELAENRG 1067
 DB 1670 NLGGKGRKNTSCPKINQFEGHFMKLQADSNVYLLSKYEYBELKQVGRNOSCDIALPENRG 1729
 QY 1068 KNRNNVLPYDISNVKLS-VQTHSTDYINANMPGHSKDFATQGPLPNTLKDTFRM 1126
 DB 1730 KNRNNILPYDATVKSINVDPCSDYINASYIRGNPFREYLVTOGPIPGTQDDFWKM 1789
 QY 1127 VMEKNVAILIMLTVCYEGRTKCEYWPSSKO--ADYGDITYAMSEIYLPMTIRDFTVK 1185
 DB 1790 VMEQNVHIVVTVQCVKGRKCDHPADDSLYGBLILQMLSESVLPMTIRREFKIC 1849
 QY 1186 NIQTSESHPL-RQHFPTSWPDHGVPTDILLINERYLVDRYMKOSPSPSPLVHCSAGV 1244
 DB 1850 GEBQDAHRLIRHHYVWPDPHGVPEITQSLIQVRVTVDRYINNSPGAGFVWCSAGVG 1909
 QY 1245 RTGFFAIDRLIYOENENTVDYGIYDLMRHPMLAVQTBQVYFLNQCYLDIVRSQXD 1304
 DB 1910 RTGFFAIDRLIQLDSDKSDYDIGAVHDLRHRVHVWQTECQYVYLHQCVRDVLRAKL 1969
 QY 1305 SKVDLIYQNTAMTIENLAP 1325
 DB 1970 RS---EQENLPEPIYENVP 1986
 RESULT 11
 ID ADO04580 standard; protein; 1997 AA.
 XX
 AC ADO04580;
 DT 15-JUL-2004 (first entry)
 XX
 DE Human HPTPbeta protein.
 XX
 KW Protein co-ordinate data; HPTPbeta; HPTP-beta; PTPRB; PTPbeta; PTPB;
 KW R-PTP-beta; angiogenesis mediated disorder; diabetic retinopathy;
 KW sickle cell anaemia; Paget's disease; mycobacterial infection;
 KW systemic lupus erythematosus; myopia; Crohn's disease; psoriasis;
 KW rheumatoid arthritis; tumour; acquired immune deficiency syndrome; AIDS;
 KW drug designing; therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004077065-A1.
 XX
 PD 22-APR-2004.
 XX
 PF 04-AUG-2003; 2003US-00634027.

XX 25-SEP-2002; 2002US-0413547P.
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 XX Evdokimov AG, Pokross ME;
 DR WPI; 2004-374235/35.
 DR N-PSDB; ADO04579.
 DR GENBANK; X54131.
 XX
 PT Identification of compound useful for treatment of angiogenesis mediated
 PT disorder, by using three-dimensional structure of HTPbeta catalytic
 PT domain, and employing structure to design, or select compound that binds
 PT HTPbeta in silico.
 XX
 PS Disclosure; SEQ ID NO 2; 335pp; English.
 XX
 CC The invention relates to the three dimensional coordinates of HTPbeta
 CC (also known as HTP-beta, PRPB, PRPBeta, PRPB or R-PRP-beta) protein. It
 CC also relates to a method for the identification of a compound useful for
 CC the treatment of an angiogenesis mediated disorder. The compounds
 CC identified by this method are useful to treat diseases like diabetic
 CC retinopathy, sickle cell anemia, Paget's disease, mycobacterial
 CC infections, systemic lupus erythematosus, myopia, Crohn's disease,
 CC psoriasis, rheumatoid arthritis, solid or blood borne tumours and
 CC acquired immune deficiency syndrome (AIDS). The invention is useful for
 CC the treatment of an angiogenesis mediated disorder or disease. It is also
 CC useful in drug design techniques. The present sequence is human HTPbeta
 CC protein.
 CC
 SQ Sequence 1997 AA;
 Query Match 17.7%; Score 1242; DB 8; Length 1997;
 Best Local Similarity 29.6%; Pred. No. 2.2e-73;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
 QY 123 FPIKXVSIPTVILWTKSNDTAASEYKVVAKHKKENKITTIVHQPCNTIGLRPATSY 182
 DB 759 FPIHVTITKNNKNTFQTSIP-----KSENE-----CVFQVLPGRLY 796
 QY 183 VFSITPGIG--NETWGDPRVYKITEPIPVSDLRVALVTVGRKAALSNGNGTASGRV 238
 DB 797 SVTVTKSGOYRANQ--GNGRTI-----PEPKDITLNRSTEDLHTWISGANG-- 844
 QY 239 LIESIGSHE--ELTODSRU-----QVNIISDLKPGVQY-----NINPYLLQSNKT 280
 DB 845 --DVDQYEIQLLFNDMKVFPFPHLVNTATEYRFTSLTPGRQYKLVLTISGVOQSAFI 901
 QY 281 KG-----DPLG-----TEGLDASN-----TERSRAGSPTAVVHDESL 313
 DB 902 EGFVTPSAVKNIHISPNQATSLTVNMTPGGDVDSYTVSAFRHSQKVDSTIIRKH---- 957
 QY 314 VGPVDPSSGQOQRDTEVLLVGLLEPGRYRNATVYSAQANGTEGQPOALEFRINAIOVDYT 373
 DB 958 -----VEHIFHRLLEAGEQYQIMIAS--VSGSLKQINIVGRITVPASVQCVI 1002
 QY 374 AVN-ISAISLILIKVSNBESSNVTYKIHVAGETSSNINVSPPRA-----VLPGL 424
 DB 1003 ADNAYSSYSLIVSQKAGVAE--RYDILLTENGILLRNTSPTATTKQHKFEDLTPGK 1059
 QY 425 RSTFTYNTVCPVADIEGTGFLQVHTPPVPVSDPFTVSTTEIGLAASHHABSFQM 484
 DB 1060 K-----YKQILTVSGGLFSKAQTEGRTPAATVLDLITENSTHLSFRWTASGELISWY 1115
 QY 485 HI---TEGAGNSRVEI--TTNQSIIIGLFPQTKYCEIIVPKGNGTEGASRTVCNRTVP 540
 DB 1116 NIFLYNDGNLOEBAQVDPVLQSFSPONLLQGRYKMWIYTH--SGLSNESPIFGRTVP 1173
 QY 541 SAVFDIHVVYVTTTE--WMLDKWSPDGASEVYVTHLVIESKGSNNTSYTDAIT---LQGL 596
 DB 1174 ASVSHLGSNKNNTDTSIMFNSPASGDF--YELLILYNPNGITKEMKDKDLTETRFQGL 1232

QY 597 IPGTLYNTISPEVDHWGDPNSTAQYTR-----PSNVSNIDVSTNTTAATL-----SMON 647
 DB 1233 VPGKTYLVAV---VTHSGDLISNKTVAESRTAPSPSLMSFADIANSTIAITWKGPDPWTD 1289
 QY 648 FDDASFTY---SYGLLIEKAGNSSNANOVVDIGITDATYVELIPSSSYVEIFAQVGDG 704
 DB 1290 YNDFELQMLPRDALTVEFPYNNKRSBGRITVG-----LPRGSSYQFNVTVSGDS 1339
 QY 705 IKSL-EPGRKSFCTDPASMASFDEEVPKPEALVIAKTCPPGANAGAELEVSAGANNAT 763
 DB 1340 WKTYSKPIFGSVTRTKPIQMLHCR--PQNSTALICSMIPDSDPDGYSIE-----CR 1390
 QY 764 HLESQSSNGREHYETWYINP-----STGNIISITTVSGGKAAPFRNCTTGIDPP 818
 DB 1391 KMDTQEVESFKLKEKESKLNTIMLVPHKRYLVSIKVQASGAMTSEVEDSTITMDRPP 1450
 QY 819 PDGSPNI-----TSVSHNSYK--VKESGFASHPIKAVAVILITG-----EAGHP 862
 DB 1451 P--PPIHRYNEKVDLIRKSSINFTVNCWSFDTNQAVKFTVVRADGSDDELKPEQHP 1508
 QY 863 SADVLKTYDDFKKASDVTYVYILIRTEKGRSQSLSEVLKYEIDVGNSTTLG----- 916
 DB 1509 LPSTLEYRHNASIRVQYTNV--FASKCAENPNSNKS----FNIKLGAWESLGKRDPT 1562
 QY 917 ---YNGKLEPIGSRACVAGFTNITPHQKGLIDGAEVYSFR--YSDA-VSLP--- 967
 DB 1563 QQKCDPPLKPHYAIRSIRAFIO-----LPD--EDLKEFTPLVSDTFSPITTT 1611
 QY 968 -QDPGVICGAVFGCIPGALVI---VTVGFIPIWRKK---RKDAKNNVSPSQIKP----- 1015
 DB 1612 ESEB--LFGAIEGVSAQLFLIGMLVANVALLIQKRVSHGRBPSARLSIRDRPLSYHL 1669
 QY 1016 -----KSKKILRVNEFEAFYFKQOADSNGCFABEYEDLKLVGISQPKYAELENRG 1067
 DB 1670 NLGQKGNRKTSCTPIKINQFGRHFMKLQADSNYLLSKREYELKDVGNOSCDIALIPENRG 1729
 QY 1068 KNRNNVLPYDISRVKLS--VQTHSTDYINANMPGVHSGKDFIATQGPLPNTLKDFFWM 1126
 DB 1730 KNRNNILPYDARVLYLSNDDPCSDYINASTIPANNRRREIYVQGLPGTKDDFFWM 1789
 QY 1127 VMEKNYAIIMLTCYBOGHTKCEEYPSKO-AQDYGDITVAMTSIIVLEWTRIDFTVK 1185
 DB 1790 VMEQVHNIMVWYQCVCEKGVKCDHWMPADQDSLYYGDILLQMLSESVLPFWTIRBFKIC 1849
 QY 1186 NIQTESHP--ROFHTSWPMDGVPPTDLLINFRVLVADYMKQSPSPESPIIVHGSAGVG 1244
 DB 1850 GEBQDLAHLIRKHFHTVWPDHGVPEFTQSLIQFRTVVDYINRSPGAGPTVHCSAGVG 1909
 QY 1245 RTGTFIALDLRYIOIENENTVDVYGLVYDLRMRPLMVQTEDOYVFLNQCVLDIVRSQKD 1304
 DB 1910 RTGTFIALDLRIIQQLDSKDSVDIYGAVHDLRLHRYVMVQTECOYVYIHQCVADVLRARL 1969
 QY 1305 SKVDLYQNTMTIYENLAP 1325
 DB 1970 RS---EOENPLPIYENVP 1986
 RESULT 12
 AAE20278
 ID AAE20278 standard; protein; 1997 AA.
 XX AAE20278;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human lung specific gene (LSG) protein #16.
 KW Human; lung specific gene; LSG; lung embryonic development; cytostatic;
 KW lung cancer; vaccine; gene therapy; non-cancerous lung disease; tumour.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers

QY	968	ODPVGICGAVNGCIGALMLVI---VTYGGFIFMRKK---RDKAKNNEVSQIAP-----	1015
Db	1612	ESBP---LFGALGVSAGVFLIGLMLVAVALLICRQKSHGGERPBARLISIRDRPLSVHL	1669
QY	1016	-----KSKFLIRVENFEAFYFKKQADSNCGFEEYEDLKVLGISOPKVAALAEVRG	1067
Db	1670	NLGGQGNKRTSGPIKINQFEGHFMLQADSNYLSKETEELKDVGRNOSCIIALLPENRG	1729
QY	1068	KRRYNNVLPYDISRYKLS-VQTHSTDDYINANMYGHSKDFIATQGLPLNTLKDFWRM	1126
Db	1730	KRRYNNILPPYDATRKYLSNVDDPCSDYINASYIFGNFRREYILTQGPLPLGTMDPFWM	1789
QY	1127	VWEKVVVALIMLTKEVQGRKCEBYWSSKQ-AQDYGGITAAMTSEYLPMTITRDPVK	1185
Db	1790	VWEQVNHNIWVQTCQEVGRVKCHYWPADDSLYGGDLIIQMSESVLPMTITREFKIC	1849
QY	1186	NIQTESHPIL-RQFHFTSMPDHGVDDTDLINFRYLVRDWMKOSPESPILVHCSGVG	1244
Db	1850	GEEQLDARLLRHFRITYTPMDHGVPETTSILQFRTYVRDYINSPGAGPVAHCSGVG	1909
QY	1245	RTGFFIALDRLLIYOIENTENVYGIYVLDLHMRPLMWQTEDQYVFLNQCLDIVRSQD	1304
Db	1910	RTGFFIALDRLLIQQLDSKDSYDIGAVHDLRLHVVHMQTEBCQYVYLHQCVRYLRKLL	1969
QY	1305	SKVDLLIYONTAAMTYENLAP	1325
Db	1970	RS---EQENLFPYEYENVP	1986

RESULT 13
ABR57179
ID ABR57179 standard; protein; 1997 AA
vv

DE	Human PTPRB protein SEQ ID NO:4.
XX	
XX	
KM	Tec; protein tyrosine kinase; protein tyrosine phosphatase; PTP10D;
KM	egg derived tyrosine phosphatase; EDRP; antidiabetic; hypotensive;
KM	cardant; antihypaemic; osteopathic; cytostatic; anorectic; obesity;
KM	immunomodulator; gene therapy; metabolic disease; eating disorder;
KM	body weight regulation disorder; cachexia; diabetes mellitus; cancer;
KM	hypertension; coronary heart disease; hypercholesterolemia; gallstone;
KM	dyslipidemia; osteoarthritis; sleep apnea; human; chromosome 12;
KM	protein tyrosine phosphatase receptor type B precursor; PTPRB.
XX	
OS	Homo sapiens.
XX	
PN	WO2003047611-A2.
XX	
PD	12-JUN-2003.
XX	
PF	04-DEC-2002; 2002WO-EP013744.
XX	
PR	04-DEC-2001; 2001EP-00128844.
XX	
PR	07-DEC-2001; 2001EP-00129138.
PR	02-JUN-2002; 2002EP-00000010.
XX	
PA	(DEVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
PI	Weise M, Eulenberk K, Fritsch R, Haeder T, Broenner G;
PI	Steuernangel A;
XX	
DR	WPI; 2003-532801/50.
DR	N-PSDB; ACC79776.
XX	
PT	New compositions comprising tyrosine phosphatase PTP10D, protein tyrosine
PT	kinase Tec or egg-derived tyrosine phosphatase genes or proteins, useful
PT	for treating or preventing metabolic diseases, e.g. as obesity or
PT	cachexia.
XX	

PS Claim 2; Fig 8B; 83pp; English.

The present invention describes pharmaceutical composition comprising a nucleic acid (I) protein tyrosine phosphatase PTP10D, non-receptor protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDTP) gene family or encoded polypeptide, fragment or variant of nucleic acid molecule or polypeptide, an antibody, an aptamer or receptor recognising a nucleic acid molecule of PTP10D, Tec, or EDTP gene family or encoded polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical composition can have antidiabetic, hypotensive, cardiac, antiplatelet, osteoprotic, cytostatic, anorectic and immunomodulator activities, and can be used in gene therapy. The composition is useful for the manufacture of an agent for detecting and/or verifying, for treating and alleviating and/or preventing a disorder, including metabolic diseases such as obesity and other body weight regulation disorders, as well as related disorders such as eating disorder, cachexia, diabetes mellitus, hypertension, coronary heart disease, hypercholesterolemia, dyslipidaemia, osteoarthritis, gallstones, cancers (cancers of the reproductive organ), sleep apnea, and other diseases (cancers of the masses, organs and/or subjects). The components of the composition may also be used in controlling the function of a gene and/or gene product which is influenced and/or modified by a PTP10D, Tec, or EDTP homologous polypeptide, and for identifying substances capable of interacting with a PTP10D, Tec, or EDTP homologous polypeptide. The nucleic acid molecule of PTP10D, Tec, or EDTP family or their fragments, may be used in the preparation of a non-human animal which over- or under-expresses the PTP10D, Tec, or EDTP gene product. The present sequence represents human protein tyrosine phosphatase receptor type B precursor (PTPRB), which is a human PTP10B homologous sequence. Human PTPRB is located to chromosome 12

SQ Sequence 1997 AA;

Query Match	17.7%;	Score 1241;	DB 7;	Length 1997;
Best Local Similarity	29.6%;	Pred. No. 2.6e-73;		
Matches 397;	Conservative 190;	Mismatches 503;	Indels 251;	Gaps 53

QY	12	PEIKAVSI--SPNNVLLIMKSNDDTAASEKVVYVKKHNEKTIYVHQPCNITGLAPATSY	182
Db	759	FDHEVITLKKNNFLQTSIP-----KSENE-----CVFQVLPGRLY	796
QY	183	VESITPGIG---NETWGDPRVIVKINERIPVSDLLVALTGVRKALWSNNGNCTASGRV	238
Db	797	SAVTATTKSGGYEANEQ--GNGRTI-----PEPVKDLTLRRSTEDLHVTTSGANG--	844
QY	239	LLESIGSHE--ELQDGRSL-----QVNIQLKPGVQY-----NINPYLLQSKMT	280
Db	845	---DVDQYEIQDLLENPKKVPPEPHLVNTATETREFTSLTGRQYKILVLTISGDVQASAFI	901
QY	281	KG-----DPLG-----TEGGLDASN-----TERSRAQSPAPVPHDESL	313
Db	902	EGFTVPSAVKNIHISPGNATDSLTVMTPEGGGDVDSTVASAFRRHQKVDSCQITPRG---	957
QY	314	VGPVDPSSGQGSRDTEVLVLGEPGRNYATVYSGAANGTEGQPAIERPTNAIQVPRVT	373
Db	958	-----VFETITPRLEAGQYQIMTAS--VSSGLKQINNVGRVTPASVQGT	1002
QY	374	AVN--ISATSLTLWKVSDNESSNYYTKIHVAGETDSNLNLYSEPPA-----VTPGL	424
Db	1003	ADNAVSSYSILVSMOKAGVAE---RYDILLTLLENGILLRNTSEPAITKOKKFEDLTGPK	1059
QY	425	RSTFNYVITCPVLGIDEGTPGFLQVHTPEPVSPRPVYVSTTEIGLAWSHDAESQIM	484
Db	1060	K-----YKIQILTVSGGLFSKEAKOTBEKRTVPAAVTDRLITENSIRHLSPRMTASGELSWY	1115
QY	485	HI---TOEGAGNSRVEI--TTNOSIILIGLPRGTQCFEIVPCKPNGTSGASRTYCNTRVP	540
Db	1116	NIFLNPNDGMLQERRAQVDPLVQSFQONLQCRMTKMYIYTH--SGELSNESPIFGRTVP	1173
QY	541	SAVEDIHVVVVLTTE--MWLDWKSPPDASXYVUHLIYESGHSNHTSYDKAII---LOGL	596
Db	1174	ASVSHLGRSNRNTTDSIMTFWMSDAGDPGF--VELLYVNPNGKLENNMKDKOLTEWPRQGL	1232

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QY 597 IPGLVNTITSPREVDHWGDPNSTAQYTR-----PSNVSNIDVSTNTAATL-----SMON 647
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1233 VPKRKVLAWY---VTHSGDLNKNVTAESRPAAPSPSLMSFADIANSTLAIWKKPDPMDT 1289
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 648 FDDASPTV---SYCLIEKAGNSSNAQVYTDITDATTTELIPSSYVEIIPAQVGDG 704
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1290 YNDFELQMLPRDALTVFNPNYNNRSEGRIVYG-----LRFGRSYOFNVTVSGDS 1339
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 705 IKSL-EBGRKSFCTDDPASMASFCEVVPKBPALVAKTCTPGANAGRELEVSASAMNAT 763
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1340 WKYYSKPIFGSVRTKPKIQNLHCR-PONSTALACSNIPDSDPDGYSIE-----CR 1390
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 764 HLESCSENGTEYRTVETVYLFN-----STSYNISITVSCGKAAAPRNTCTTGITDPP 818
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1391 KMDTQVEFSPKLEKEKESLNNIMLVPHKRYLVSITKVSAGMSEVVEDSTITMIDRPP 1450
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 819 PDGSPNI-----TSVSHSVK--VKFSGPASHGPIKAVAVIITG-----EAGHP 862
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1451 P--PPIHVRNEKDVLLSKSSINFVNCWFSDDTGAVKYFTVVVREAGSDDELKPEQHP 1508
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 863 SADVLTQYDFFKKGASDVTYVTLIRTEEKGSGSLSEVLKYEIDVGNSTTG----- 916
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1509 LPSYLEIRRHNASIRVYQTNV--FASKCAENPNSNKS---FNKLAEMESLGGKCDPT 1562
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 917 ---YNGKLEPLSGYRACVAGFTNITFHPQNGKIDGAEYSVFSR--YSDA-VSLP--- 967
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1563 QAKFCSGPKLPHTRAYRISIRAFQ-----LFD--EDUKETKLYLSDTFPSLITTT 1611
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 968 -QDPGVCIGAVFGCIFGALVI---VTVGSPITWKK--RKDAKNNEVSFSQIKP----- 1015
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1612 ESEPP--LFGAIEGVSAQLFLIGMLVAVALLICQKQVSHGERSARLSIRDRPLSVHL 1669
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1016 -----KSKLIRVNFPAFYKQOQADNSCGFAEYEDLKIVGISQPKYAAFLASNRG 1067
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1670 NLQCKGNKRTSCPKLQNFEGHFMKQADSNVYLSLSEKLDVGRNQCSDIALPENRG 1729
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1068 KNRVNNVLPYDISRVKLS-VQTHSTDDYINANVMPGYSKKDFATQGPLPNTLKDPWRM 1126
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1730 KNRVNNVLPYDARVKSNDVDDPCSDYINASYIPGNFRREYLVITGSLPGLTDDPWKM 1789
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1127 VMEKNVYAIIMLTVCVQGRTKCEEYPSKO-AQDYGDITVAMTSEIVLPEMTIRDTVK 1185
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1790 VMEKNVYAIIMLTVCVQGRTKCEEYPSKO-AQDYGDITVAMTSEIVLPEMTIRDTVK 1849
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1186 NITQSEHNP--ROHFTSPMDHGVPTDILLINRYLVROYMKSPPESPLVHCSAGVG 1244
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1850 GEEQDLAHLRIHFHYVWPDPHGVETTSLOQFVRTROYINKSPAGPVAHCSAGVG 1909
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1245 RTGTFIADRLIYOIEBENTVDVYGYVLDLMEHRLPLAVQTEDOYVFVNOCVLIVRSQD 1304
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1910 RTGTFIADRLIYOIEBENTVDVYGYVLDLMEHRLPLAVQTEDOYVFVNOCVLIVRSQD 1969
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1305 SKVDLYQNTAMTAMTENTAP 1325
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1970 RS----EQENPLFPIYENVP 1986
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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KM osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
XX W02003087768-A2.
XX
XX 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
XX
XX 17-JUN-2002; 2002US-0389987P.
XX
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
XX
XX (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW,
XX Warnock DE;
XX
XX WPI; 2003-845369/78.
XX
XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX with the disease.
XX
XX Claim 1; SEQ ID NO 2135; 180pp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
XX for therapeutic intervention in treating a disease associated with
XX altered mitochondrial function. Specifically, it refers to a method for
XX identifying proteins of the human heart mitochondrial proteome that are
XX useful for drug screening assays, as well as therapeutic targets. The
XX present invention describes a method for identifying such proteins that
XX can be used in the treatment of various diseases associated with altered
XX mitochondrial function including diabetes mellitus, Huntington's disease,
XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX compositions have neuroprotective, nootropic, antidiabetic,
XX anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX cytoskeletal activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.
XX
XX Sequence 1997 AA;
XX
XX Query Match 17.7%; Score 1241; DB 7; Length 1997;
XX Best Local Similarity 29.6%; Pred. No. 2.6e-73;
XX Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
QY 123 PDKAVSISPTNVILTKSKNDTAASEKYVYKAKMEKEKITTIVHQCWNITGRPATSY 182
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 759 FDHYEYTIKKNKNFQTKSIP-----KSENE-----CVFVQLVPGRLY 796
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 VFSITPGIG---NETMGDPRLVKVITEPIVPSDLRVALGVKRAALSWNGNCTASCRV 238
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 797 SVTVTKSGQYEAEQ-NGRGTI---PEVADLTIRNSTEDLHVTWGSANG----- 844
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 LLESIGSHE--ELTQDSRL-----QVNSIDLKPGVOY-----NINPYLQSNKT 280
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 845 ---DVQDEYQLFNDMKVFPFHLVNTATBYRTSLTPGRQYILVLITSGDVQGAFI 901
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 281 KG-----DPLG-----TBGGLDASN-----TERSAQSPFAVHDESL 313
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 902 EGFTVPQAVNKHINISPGADTSLVNMWTPGSGVDVTSVSAFRUSQVDSQITIPKH---- 957
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 314 VGFPDPSSGGQNSDTEVLVLGLBPGTRVYNAVTVYSGAANGTEGQQAIEPTNAIQVDYT 373
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 958 -----VFETTHRLBNGEYOYQIMIS--VSGSLKQOINVAGRTVPASVGV 1002
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 374 AVN-ISATSLTLVWKVSDNESSNVTYTKIHVAGETDSNLNVSEPPA-----VTPGL 424
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```



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Db 1003 ADNAVSYSLIYSWOKAGVAB---RYDILLITLNTENGILLRNTSEPAATKQHKFEIDLTPGK 1059
Qy 425 RSSTFYNTITCPVLADIEGTPGLQVHTPPVPSDRYRVVSTTELGAMSHHDESPQM 484
Db 1060 K-----YKIQILTVSGGLFSKKAQTEGRTVPAVATDILITENSTRLHSFEFWTSEBELSMY 1115
Qy 485 HI---TOEGAGNSRVEI--TTNOSIIGLLEFGTKYCFEIVPQPGNTEGASRTVCNRTVP 540
Db 1116 NIFLYPNPDNLQERAGVDPLVQSFQNLQGRMYGVIVTH--SGELSNSEFIRGRYVP 1173
Qy 541 SAVFEDIHVVYVTTTE--MWDKMSPDGASVYVHLVIESKGSNHTSTYDKAIT---LOGL 596
Db 1174 ASVSHLRGSRNNTTSLMFMNMSPDAGDFP--YELLVYNGNKGKKNWQKDLTEWRFQGL 1232
Qy 597 IEGTLNITISPEVDHVMGDPNSTAQYTR-----PSNVSNIDVSTNTTAATL-----SMON 647
Db 1233 VPGKRYVLWV---VTHSGDLNKKVTAESTAPSPSLMSFADIANTSLAITKGPDPWTD 1289
Qy 648 FDDASPTT---SYCLIEKAGNSNATQVYVDIGITDAVTLELLPGSSYVTEIFAQVGDG 704
Db 1290 YNDFELOWLPRDALTVFNPNYNRKSEGRIVYG-----LRGRSGYQFNVKTVSGDS 1339
Qy 705 ISL--EPGRKSFCTDPASMSAFDCEVVPREPALVLTCTCPRANAGFELEVSQAMANNAT 763
Db 1340 WKTYSKPIFGSVTRKPDCKIQNHCR--PONSTALACSWLPPSDDFDYSIE-----CR 1390
Qy 764 HLESCSSENGTEYRTEVYTLNF-----STSYNISITTVSCGMKAPANTCTGTTDPP 818
Db 1391 KMDTQEVFSRKLKREKSLNIMMLVPHKRYLVSIKVQAGMTSVVSDSTITIMIDRPP 1450
Qy 819 PDGSPNI-----TSVSNYSVK--VKFSGFASHPPIAIVAVILTTG-----EAGHP 862
Db 1451 P--PHIIVNKKDVLISKSSINFTVNCWFSFDPINCAVYFTVYVREADGSDLEKPEQHP 1508
Qy 863 SADVLKTYTDDFKKASDPTVYTYLIRTEKRSOSLSVLYKXELDVGNSTTLG----- 916
Db 1509 LPSYLEYHNHNASIRYQYQNY--FASKCAENPNNSKS-----FNKLGAMSLGCKDPT 1562
Qy 917 ---YNGCLEPLGSTRACVAGTNTTFHPQNKGLIDGASVYFSR--YSDA-VSLP--- 967
Db 1563 QQKCFDGLPKPHTYRISIRAFDQ-----LFD--EDLKFTKPLYSDFPSLPTT 1611
Qy 968 -ODPGVIGAVGCGIFGALVI---VTYGGFIWFKK---RDKAKNVSFSQIRP----- 1015
Db 1612 ESEF--LFGALIEGYSAGLFLIGMLVAVVALICQOKVSHGERPSARLSIRDRPLSVHL 1669
Qy 1016 -----KSKKLIRVENFEAYFKKQADSNCGFAEYEDIKVIGISQPKYAAELAENRG 1067
Db 1670 NLGQKGNRKTCSPKIKINQFEGHFMKQLQADSVYLLSKYEELKQVGRNOSCDIALPENRG 1729
Qy 1068 KNRNANNLPYDISVKYS--VQTHSTDYINANNWPGHSHKKDFTATQGPLPNTLKDFWM 1126
Db 1730 KNRNANNLPYDATTVKLSNVDDDPCSDYINASYIPGNNFREYLVTOGSPFGTKDDFWKM 1789
Qy 1127 VMEKNVVAIIMLTQVCEGRTKCEYWPSCO--ADQYDIDIVAMSEIVLEBMTIRDPYVK 1185
Db 1790 VMEQNVNINIVAVTQVCEKGRKCHMYPAODDSLYTGBLLQMLSESVLEBMTIREKXIC 1849
Qy 1186 NIGTSESHPL-RQHTFSWPDHGVDTTDLINERLVLDYMKQSPPEPILVHCSAGVG 1244
Db 1850 GEEOLDHRLRHRHHTVWPDHGVETTQSLIGFVRVDRDYINRSPAGPTVHCSAGVG 1909
Qy 1245 RTGFEIADRLIYIENBNVYVGIYDLMRPRLMVQVEDQVFLNQCVLDIVSQQD 1304
Db 1910 RTGFEIADRLIYIENBNVYVGIYDLMRPRLMVQVEDQVFLNQCVLDIVSQQD 1304
Qy 1305 SKVDLIYQNTAMTIYENLAP 1325
Db 1970 RS-----EQENPLPFIYENVNP 1986

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RESULT 15
AAM79805

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ID AAM79805 standard; protein; 2002 AA.
XX AC AAM79805;
XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3451.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200157190-A2.
XX PD 09-AUG-2001.
XX PF 05-FEB-2001; 2001WO-US004098.
XX PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
XX PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
PI Xue J, Yang Y, Wejrtman T, Goodrich R,
XX WPI; 2001-476283/51.
XX DR N-PSDB; AAK52938.
XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX PS Claim 20; Page 340-341; 6221pp; English.
XX XX
XX The invention relates to polynucleotides (AAK51456-AAK51435) and the
XX encoded polypeptides (AAM78923-AAK80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibitin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication.
XX
SQ Sequence 2002 AA;
Query Match 17.7%; Score 1241; DB 4; Length 2002;
Best Local Similarity 29.6%; Pred. No. 2,6e-73;
Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
Qy 123 FDKAVSISPTVILTWKSNTPAASEYKVVYKHKMKNKTTTVHQPNCNITGLRPATSY 182
Db 764 PDHYEVITKANKNPFQYTSIP-----KSENE-----CYFVQVLPGLY 801
Qy 183 VFSITPGIG---NETWGDPRVIVKITEPIVPSDLRVALTGVRAALSWSNNGNCTASC RV 238
Db 802 SVTVTTKSGQYEAENQ--GNGRTI-----PEPVKQULTLRNSTEDLHTWGSANG----- 849
Qy 239 LLESTGSHE--ELTQDSRL-----QVNSIDLKPGVQY-----NINPYLLQSNKT 280

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Db	850	---	DVDQ	IEI	OLL	FN	DM	KV	FP	FP	PH	LV	NT	AT	IE	RT	FS	LT	PK	Q	KL	VL	IT	SG	VD	QA	S	FI	906																									
Qy	281	KG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	313																									
Db	907	EG	FT	PA	SV	AK	NI	HS	PN	GA	TD	SL	VT	MT	PG	GD	VD	SV	VA	FR	HS	Q	VD	ST	PI	PK	----	962																										
Qy	314	VGP	VD	PS	SG	Q	S	R	D	T	EV	LV	GL	E	P	CT	R	NA	VT	Y	S	O	A	N	G	T	E	G	O	PA	I	E	FR	NA	I	Q	VD	Y	373															
Db	963	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1007																									
Qy	374	AV	N	-	IS	AT	SL	TI	M	V	VS	D	N	ESS	N	AT	Y	K	I	H	A	G	E	T	D	S	N	L	V	SP	RA	-----	VI	P	GL	424																		
Db	1008	AD	NA	Y	S	S	I	S	L	V	S	W	Q	A	KA	GV	AB	--	RY	I	L	L	T	ENG	I	L	NT	S	E	BA	TT	K	H	E	D	L	T	PG	1064															
Qy	425	RS	TF	Y	N	T	IT	VC	P	VL	GD	IE	GT	PG	F	L	Q	W	HT	P	P	V	P	S	D	FR	V	T	V	S	T	E	I	G	L	AM	S	HA	E	S	FO	M	484											
Db	1065	K	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1120																									
Qy	485	HI	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	540																										
Db	1121	NI	FL	Y	N	P	D	GN	I	Q	E	RA	Q	VD	P	L	V	Q	S	F	Q	N	L	O	GR	MY	K	AV	I	Y	H	--	S	G	E	L	N	E	S	E	I	FG	RT	P	1178									
Qy	541	SA	VP	D	I	H	V	V	Y	T	T	E	--	M	L	D	M	K	S	P	D	G	A	S	E	V	Y	H	I	V	E	S	K	S	N	H	T	S	T	D	K	A	I	T	---	LO	GL	596						
Db	1179	AS	V	SH	L	R	G	S	N	R	N	T	D	S	L	T	W	F	M	N	S	P	A	S	G	D	D	P	--	Y	E	L	L	Y	N	P	N	G	T	K	E	M	X	D	OL	T	W	R	P	Q	GL	1237		
Qy	597	I	P	G	L	Y	N	T	I	S	P	E	V	D	H	V	M	G	D	N	S	T	A	Q	Y	T	R	-----	P	S	N	S	N	I	D	V	E	N	T	T	A	A	T	---	SW	ON	647							
Db	1238	V	P	G	R	K	Y	V	L	M	V	---	V	H	S	G	D	L	S	N	K	T	Y	A	E	R	T	A	P	S	P	S	L	M	S	F	A	D	I	N	T	S	L	A	I	T	W	K	P	P	M	T	D	1294
Qy	648	F	D	D	A	S	P	T	---	S	T	C	L	L	E	K	A	G	N	S	N	A	I	Q	V	T	D	I	G	T	D	I	T	A	T	T	E	L	L	P	G	S	S	Y	E	I	F	A	Q	VD	G	704		
Db	1295	Y	N	D	E	L	Q	M	L	P	R	D	A	L	T	V	F	N	P	N	N	R	K	S	E	G	R	I	V	G	-----	L	R	G	S	Y	O	F	N	V	T	S	G	D	S	1344								
Qy	705	I	K	S	L	-	E	P	R	K	S	F	C	D	P	A	S	M	A	F	D	E	V	N	P	K	E	A	L	V	L	K	M	T	C	P	R	G	A	N	A	F	E	L	E	V	S	G	A	M	N	A		

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Db      1855  GEEGLDARHLRIHRYHYVWPHGVPEFTQSLIGFVRTRVDYINNSPGCGPVTWCSAUG 1914A
Oy      1245  RTGFIFILDIRLYOENENTVDYGIYDLBMNHPLWVQTEDEQVYFLNQCYLDIRSOKD 1304A
Db      1915  RTGFIFILDIRLYOQDSDSDYDIGAHHDLRLHRYVHVQTEQCYVYLHQCGRDYLARKL 1974A
Oy      1305  SKVDLIYQNTAMTYENLAP 1325
Db      1975  RS---EENDELPFIYENVP 1991

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Search completed: May 10, 2005, 19:01:24
Job time : 210 secs

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Db      1855  GEEQLDAHRLIRHPHYTWMPDHGVPEFTQSLIQFVRTVRDYINRSPGAGPTVHCSAGVG 1914
OY      1245  RTGTFIAIDRLIYIENENTVDTYGIYDLMHRPLMWQTEDOYVEFLNQCVLDIVRSQXD 1304
          |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1915  RTGTFIALDRILQOLDSKDSVDYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLRARKL 1974
OY      1305  SKVDLIYONTTAMTIYENLIAP 1325
          |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1975  RS---EOENPLFPIYENVNP 1991

Search completed: May 10, 2005, 19:01:24
Job time : 210 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:57:02 ; Search time 46 Seconds
(without alignments)
2169.691 Million cell updates/sec

Title: US-09-516-728A-4

Perfect score: 7030
Sequence: 1 MKPAREARLPFRSPGRLMA.....TIYENLAPYTFKNGYIA 1337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
 - 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
 - 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
 - 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
 - 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	6824	97.1	1337	US-08-854-585-2	Sequence 2, Appli
2	6824	97.1	1337	US-09-447-533-2	Sequence 2, Appli
3	6824	97.1	1337	PCT-US95-05512-2	Sequence 2, Appli
4	1242	17.7	1997	US-09-949-016-6275	Sequence 6275, Ap
5	1241	17.7	1903	US-09-949-016-8049	Sequence 2, Appli
6	954	13.6	1711	US-08-342-930-2	Sequence 2, Appli
7	864	12.3	2301	US-09-822-871-4	Sequence 4, Appli
8	855	12.2	1188	US-08-201-697-4	Sequence 4, Appli
9	854	12.1	1246	US-09-949-016-8051	Sequence 8051, Ap
10	854	12.1	1246	US-09-949-016-8052	Sequence 8052, Ap
11	854	12.1	1246	US-09-949-016-8053	Sequence 8053, Ap
12	854	12.1	1246	US-09-949-016-8054	Sequence 8054, Ap
13	854	12.1	1246	US-09-949-016-8055	Sequence 8055, Ap
14	842	12.0	1187	US-08-201-697-2	Sequence 2, Appli
15	841	12.0	1274	US-09-949-016-8828	Sequence 8828, Ap
16	841	12.0	1274	US-09-949-016-8829	Sequence 8829, Ap
17	841	12.0	1274	US-09-949-016-8830	Sequence 8830, Ap
18	841	12.0	1274	US-09-949-016-8831	Sequence 8831, Ap
19	841	12.0	1274	US-09-949-016-8832	Sequence 8832, Ap
20	833.5	11.9	2278	US-08-201-697-16	Sequence 16, Appli
21	826	11.7	2291	US-08-822-871-2	Sequence 2, Appli
22	815.5	11.6	1911	US-08-348-006B-5	Sequence 5, Appli
23	815.5	11.6	1911	US-08-800-825A-5	Sequence 5, Appli
24	815.5	11.6	1911	US-09-158-657-5	Sequence 5, Appli
25	815.5	11.6	1911	PCT-US94-10166-5	Sequence 5, Appli
26	785.5	11.2	1452	US-08-652-971-4	Sequence 4, Appli
27	785.5	11.2	1452	US-08-991-258A-4	Sequence 4, Appli

28	785.5	11.2	1452	2	US-08-769-399-4	Sequence 4, Appli
29	785.5	11.2	1452	3	US-08-991-953A-4	Sequence 4, Appli
30	778.5	11.1	1254	2	US-08-685-992-14	Sequence 14, Appli
31	778.5	11.1	254	2	US-09-144-925-14	Sequence 14, Appli
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34	748	10.6	898	1	US-08-036-210-22	Sequence 22, Appli
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36	748	10.6	898	4	US-09-361-096A-22	Sequence 22, Appli
37	742.5	10.6	1501	2	US-08-447-464-3	Sequence 3, Appli
38	742.5	10.6	1501	2	US-08-716-679-3	Sequence 3, Appli
39	737.5	10.5	506	4	US-09-949-016-8833	Sequence 8833, Ap
40	737.5	10.5	506	4	US-09-949-016-8834	Sequence 8834, Ap
41	737.5	10.5	506	4	US-09-949-016-8835	Sequence 8835, Ap
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43	737.5	10.5	506	4	US-09-949-016-8837	Sequence 8837, Ap
44	737.5	10.5	506	4	US-09-949-016-8838	Sequence 8838, Ap
45	720.5	10.2	1075	4	US-09-949-016-8308	Sequence 8308, Ap

ALIGNMENTS

RESULT 1
US-08-854-585-2
Sequence 2, Application US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and Stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-585-2
Query Match 97.1%; Score 6824; DB 3; Length 1337;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;
Cy 1 MKPAREARLPFRSPGRLMLPLLLLRGQILCAGTSPSPDPSPVAVATGNGITQ 60
Db 1 MKPAREARLPFRSPGRLMLPLLLLRGQILCAGTSPSPDPSPVAVATGNGITQ 60
Cy 61 ISSFAEFHKGNGTGTQVETNTSEDESSGANDSLRTPGSGNGTGDAGQKTPSSTGPS 120

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Db      61  ISSTASFHKONGIGTPOVETNTSDEGSSGANDSLRTPGSGNGTDGASQKTPSSGTGS 120
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Db      121  PVEDIKAVSISPTNVILITWKSNDTAASEYKYVYKHKMENEKTIIVYHQWCNITGLRPT 180
Qy      181  SYVFSITPGIGNETWGDPRVIAKITEPIPVSDLRVALTGVRKALSMNGNGTASGRVLL 240
Db      181  SYVFSITPGIGNETWGDPRVIAKITEPIPVSDLRVALTGVRKALSMNGNGTASGRVLL 240
Qy      241  ESTGSHBELTQDRLQVNIISDLKPGVQVNIINPYLLOSNTKGDPLGEGGLDASNTESR 300
Db      241  ESTGSHBELTQDRLQVNIISDLKPGVQVNIINPYLLOSNTKGDPLGEGGLDASNTESR 300
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Db      301  AGSPITAPVHDESLVGPVDPSSGOOSRDETVLVGLGEPGRNATYVYSCAANGTEGQPAI 360
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Db      361  EFRTNALQVFDVTAVNIISATSLTLTWKSDNESSSNYYTKIHVAGETDSNINVEPRAY 420
Qy      421  IGLRSTERYNTVCGVLDIGTREGLOVHTPPVPVDFRTVYVSTTEIGLAWSSHDAE 480
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Qy      481  SFQOMHITQEGAGNSRVEITTNOSIIIGLFPETKXCFEIVPKPGNGTGASRTVGNRTVP 540
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Qy      541  SAVFIHVVYVYTTTETMLDMKSPDGASEYVYHVLIESKHGSHNISTYKAITLQGLIPGT 600
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Qy      601  LYNTITSEVDHVMGDPNSTAQTPTPSNVNSINDVSTNTTAATLSQONQNDASPTYSYLL 660
Db      601  LYNTITSEVDHVMGDPNSTAQTPTPSNVNSINDVSTNTTAATLSQONQNDASPTYSYLL 660
Qy      661  IEKAGNSSNATQVVDIGITDATTVELIPGSSYVELFAQVGDGKSLPERKSFCTDPA 720
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Qy      721  SMAFDCVPEKPEPLVTKTCPPRANAGFELEVSAGANNATHESSCSNGEYRTREV 780
Db      721  SMAFDCVPEKPEPLVTKTCPPRANAGFELEVSAGANNATHESSCSNGEYRTREV 780
Qy      781  TYLNFSTSYNISITTVSCGMAAPTRNTCTGITDPPPPGSPNITSYSHSVKXSGF 840
Db      781  TYLNFSTSYNISITTVSCGMAAPTRNTCTGITDPPPPGSPNITSYSHSVKXSGF 840
Qy      841  EASHGPICAYAVILITGAGHPADVLKTYTDDFKGASDTTYVYLIRTEBKRSQSLSE 900
Db      841  EASHGPICAYAVILITGAGHPADVLKTYTDDFKGASDTTYVYLIRTEBKRSQSLSE 900
Qy      901  VLKTEIDVGNSTLIGYNGKLEBPLGSRACVAFNTITHPQKGLIDGAESEVVSRY 960
Db      901  VLKTEIDVGNSTLIGYNGKLEBPLGSRACVAFNTITHPQKGLIDGAESEVVSRY 960
Qy      961  SDAVSLPQDPGVICGAVGCIFGALVITVGGFIFMKKGRKDAONNVVSQIKPKSKL 1020
Db      961  SDAVSLPQDPGVICGAVGCIFGALVITVGGFIFMKKGRKDAONNVVSQIKPKSKL 1020
Qy      1021  IRVENFEAYFKKQADNSCGFAEYEDLKVGISQPKYAAFLAENGRKRNVLPRDIS 1080
Db      1021  IRVENFEAYFKKQADNSCGFAEYEDLKVGISQPKYAAFLAENGRKRNVLPRDIS 1080
Qy      1081  RVKLSVQTHSTDDYINANMYGYSKDOFIATQSPFLNTLKDPRWMEGNVVAIIMLTK 1140
Db      1081  RVKLSVQTHSTDDYINANMYGYSKDOFIATQSPFLNTLKDPRWMEGNVVAIIMLTK 1140
Qy      1141  CVEGGRKCEBYWPSKQADYGDITVAMTSEIYLPWTIRDFYVKNIQTSSEHPLRQPHF 1200

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Db      1141  CVEGGRKCEBYWPSKQADYGDITVAMTSEIYLPWTIRDFYVKNIQTSSEHPLRQPHF 1200
Qy      1201  TSPMDHGVPTDTLLINFRYLVRDYMKQSPESPILVHCSAGVGTGFLAIDRLIYQIE 1260
Db      1201  TSPMDHGVPTDTLLINFRYLVRDYMKQSPESPILVHCSAGVGTGFLAIDRLIYQIE 1260
Qy      1261  NENTVDYGIYDILRMHREPLMVQTEQDYVFLNQCVDIVSOKSKVDLIYQNTAMTIY 1320
Db      1261  NENTVDYGIYDILRMHREPLMVQTEQDYVFLNQCVDIVSOKSKVDLIYQNTAMTIY 1320
Qy      1321  ENLAPVTTFGKTINGYIA 1337
Db      1321  ENLAPVTTFGKTINGYIA 1337

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RESULT 2
US-09-447-533-2
; Sequence 2, Application US/09447533
; Patent No. 6552169
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K.
;
; Oeltnan, Arne
TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
PHOSPHATASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group PLLC
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,533
FILING DATE: 23-No. 6552169-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Roseman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200125, 402C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-447-533-2

```

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Query Match      97.1%; Score 6824; DB 4; Length 1337;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;
Qy      1  MKPAREARLPFRSGLRWALPLLLLLRLQGIICAGGTPSPIDPSVATVATGNGITQ 60
Db      1  MKPAREARLPFRSGLRWALPLLLLLRLQGIICAGGTPSPIDPSVATVATGNGITQ 60
Qy      61  ISSTASFHKONGIGTPOVETNTSDEGSSGANDSLRTPGSGNGTDGASQKTPSSGTGS 120
Db      61  ISSTASFHKONGIGTPOVETNTSDEGSSGANDSLRTPGSGNGTDGASQKTPSSGTGS 120
Qy      121  PVEDIKAVSISPTNVILITWKSNDTAASEYKYVYKHKMENEKTIIVYHQWCNITGLRPT 180
Db      121  PVEDIKAVSISPTNVILITWKSNDTAASEYKYVYKHKMENEKTIIVYHQWCNITGLRPT 180

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Qy 181 SYFSTIPGIGNETWGPRIYKVTBEPVSDLRVALTVGRKALSWNSNGTASCRVLL 240
Db 181 SYFSTIPGIGNETWGPRIYKVTBEPVSDLRVALTVGRKALSWNSNGTASCRVLL 240
Qy 241 ESIGSHELTQDSRLQVNIISDLKPGVOYNINPYLLQSNKTKGDPGLTEGGGLDASNTSR 300
Db 241 ESIGSHELTQDSRLQVNIISDLKPGVOYNINPYLLQSNKTKGDPGLTEGGGLDASNTSR 300
Qy 301 AGSPRTAVHDESLVGPVDPSSGQSRDTEVLLVGLBEGTRNATVYQOANGTEGQPOAI 360
Db 301 AGSPRTAVHDESLVGPVDPSSGQSRDTEVLLVGLBEGTRNATVYQOANGTEGQPOAI 360
Qy 361 EPTNAIQVFDVAVNISATSLTLIMKVDNESSNTYKIHVAGETDSNLTANSEPRAY 420
Db 361 EPTNAIQVFDVAVNISATSLTLIMKVDNESSNTYKIHVAGETDSNLTANSEPRAY 420
Qy 421 IPGLRSTFYNTVCPVLGDIEGTGFGLQVHTPPVPSDFRTVVSITTEIGLAWSHDAE 480
Db 421 IPGLRSTFYNTVCPVLGDIEGTGFGLQVHTPPVPSDFRTVVSITTEIGLAWSHDAE 480
Qy 481 SPQWHTIOEGAGNSRVEITTNQSIIGGLPFGTKYCEIYVPGKNGTEGASRTVCARTVP 540
Db 481 SPQWHTIOEGAGNSRVEITTNQSIIGGLPFGTKYCEIYVPGKNGTEGASRTVCARTVP 540
Qy 541 SAVFDIHVVYVTTTMMMLDMKSPDGASEVYVHLVIESKGSNHTSTYDKAITLQGLPGT 600
Db 541 SAVFDIHVVYVTTTMMMLDMKSPDGASEVYVHLVIESKGSNHTSTYDKAITLQGLPGT 600
Qy 601 LYNITISPEVDHVMGDNPSIAQYTRPSNVSNIDVSTNTAATLSWQNFDDASPTYSYCLL 660
Db 601 LYNITISPEVDHVMGDNPSIAQYTRPSNVSNIDVSTNTAATLSWQNFDDASPTYSYCLL 660
Qy 661 IERKAGNSNATQVVTGIDTATYELLPGSSYVVEI PAQVGDGDKISLEPERKSCFCDPA 720
Db 661 IERKAGNSNATQVVTGIDTATYELLPGSSYVVEI PAQVGDGDKISLEPERKSCFCDPA 720
Qy 721 SMASFDDEVVPKEBALVLTCTCPPGANAGFLEVSAGANNATLHSCSSNGTEYRTV 780
Db 721 SMASFDDEVVPKEBALVLTCTCPPGANAGFLEVSAGANNATLHSCSSNGTEYRTV 780
Qy 781 TYLNFTSYNISITTVSCGMAAPTRNTCTTGTPPPDGSPIITSVSHNSVVKVSGF 840
Db 781 TYLNFTSYNISITTVSCGMAAPTRNTCTTGTPPPDGSPIITSVSHNSVVKVSGF 840
Qy 841 EASHGPIKAAVAVILITTEBAGHPADVLKTYDDPKKASDITYTYLLIRTEKGRSQSLSE 900
Db 841 EASHGPIKAAVAVILITTEBAGHPADVLKTYDDPKKASDITYTYLLIRTEKGRSQSLSE 900
Qy 901 VLKKEIDVGNESFTLGYYNGKLBPLGSYRACVAGFTNITPHQKGLIDGAEVYSFSRY 960
Db 901 VLKKEIDVGNESFTLGYYNGKLBPLGSYRACVAGFTNITPHQKGLIDGAEVYSFSRY 960
Qy 961 SDAVSLPQDQGVLCGAVFGCIFGALVITVVGFI FMRKKRKAONNEVSFSQIKPKSKL 1020
Db 961 SDAVSLPQDQGVLCGAVFGCIFGALVITVVGFI FMRKKRKAONNEVSFSQIKPKSKL 1020
Qy 1021 IRVENFAIRFKKQADSNCGAEBEYEDLKVGISQPKYAAELAKNGKRNANVLPDIS 1080
Db 1021 IRVENFAIRFKKQADSNCGAEBEYEDLKVGISQPKYAAELAKNGKRNANVLPDIS 1080
Qy 1081 RYKLSVQTHSTDDYINANNVYGYSKKOPIATQGPLPNTLKDPRMWEKKNVYAIIMLTK 1140
Db 1081 RYKLSVQTHSTDDYINANNVYGYSKKOPIATQGPLPNTLKDPRMWEKKNVYAIIMLTK 1140
Qy 1141 CVBQGRTRKCEBYWPSKQADQDITVAMTSEI VLPWTIRDPYKNIQTSESHPLRQHF 1200
Db 1141 CVBQGRTRKCEBYWPSKQADQDITVAMTSEI VLPWTIRDPYKNIQTSESHPLRQHF 1200
Qy 1201 TSWPDHGVPTDTLLINFRYLYRDYMQSPESPESILVHCSAGVGRGFIADILYQIE 1260
Db 1201 TSWPDHGVPTDTLLINFRYLYRDYMQSPESPESILVHCSAGVGRGFIADILYQIE 1260
Qy 1261 NENTVDVYGIYDLMRMRPLMWQTEQDQVFLNQCVLDIVRSQKSKVDLIYQNTTAMTIY 1320

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Db 1261 NENTVDVYGIYDLMRMRPLMWQTEQDQVFLNQCVLDIVRSQKSKVDLIYQNTTAMTIY 1320
Qy 1321 ENLAPVTTFGKNGXYIA 1337
Db 1321 ENLAPVTTFGKNGXYIA 1337

RESULT 3
PCT-US95-05512-2
Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael P.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05512-2

Query Match 97.1%; Score 6824; DB 5; Length 1337;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MKPAAERARLPSPSGRLMALPLILLRLGQIICAGGTSPPIRDPVSATVATGNGITQ 60
Db 1 MKPAAERARLPSPSGRLMALPLILLRLGQIICAGGTSPPIRDPVSATVATGNGITQ 60
Qy 61 ISSAESFHKONGTGTPVETNTSEDESSGANDSLRTPREGSNGTGAOSKTPSTGPS 120
Db 61 ISSAESFHKONGTGTPVETNTSEDESSGANDSLRTPREGSNGTGAOSKTPSTGPS 120
Qy 121 PVFDIKAVSISPTNVILTWKSNDRPAASEYKVVYGHKMEKNTITVYHQPCNITGLBPAT 180
Db 121 PVFDIKAVSISPTNVILTWKSNDRPAASEYKVVYGHKMEKNTITVYHQPCNITGLBPAT 180
Qy 181 SYFSTIPGIGNETWGPRIYKVTBEPVSDLRVALTVGRKALSWNSNGTASCRVLL 240
Db 181 SYFSTIPGIGNETWGPRIYKVTBEPVSDLRVALTVGRKALSWNSNGTASCRVLL 240
Qy 241 ESIGSHELTQDSRLQVNIISDLKPGVOYNINPYLLQSNKTKGDPGLTEGGGLDASNTSR 300
Db 241 ESIGSHELTQDSRLQVNIISDLKPGVOYNINPYLLQSNKTKGDPGLTEGGGLDASNTSR 300
Qy 301 AGSPRTAVHDESLVGPVDPSSGQSRDTEVLLVGLBEGTRNATVYQOANGTEGQPOAI 360

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Db 301 QGAPPLCMMSPFVGPVDPSSGOOSRDTEVLVLGEPGTRYNATVYSQANGETGQPOAI 360
Qy 361 EFRTNALQVEDYATVANNISATSLTLIMKVSNDNESSNVTYKIHAGETDSNINVSPPRAY 420
Db 361 EFRTNALQVEDYATVANNISATSLTLIMKVSNDNESSNVTYKIHAGETDSNINVSPPRAY 420
Qy 421 IPELRSTFNITVCPVLGDIESTPGFLOVHPVPVSDPRVTVSTTEIGLAMSHDAA 480
Db 421 IPELRSTFNITVCPVLGDIESTPGFLOVHPVPVSDPRVTVSTTEIGLAMSHDAA 480
Qy 481 SFQMHITQEGAGSRVEITNOSIIIGLPGTKYCFEIVPGMGTGASRTVCNRYTP 540
Db 481 SFQMHITQEGAGSRVEITNOSIIIGLPGTKYCFEIVPGMGTGASRTVCNRYTP 540
Qy 541 SAVFDIHVVYVTTTMMMDKSPDGASEYVYHLVIESKGSNHTSYDAITLQGLIPGT 600
Db 541 SAVFDIHVVYVTTTMMMDKSPDGASEYVYHLVIESKGSNHTSYDAITLQGLIPGT 600
Qy 601 LKNTITSEVVDHWGDPNSTAQYTRPSNVSNIDVSTNTTAAITLSQNFDDASPTYSYCL 660
Db 601 LKNTITSEVVDHWGDPNSTAQYTRPSNVSNIDVSTNTTAAITLSQNFDDASPTYSYCL 660
Qy 661 IEKAGNSNATQVVDIGITDAITVELIPGSSYVEIFQVGDGKSLERGRKSCCTPA 720
Db 661 IEKAGNSNATQVVDIGITDAITVELIPGSSYVEIFQVGDGKSLERGRKSCCTPA 720
Qy 721 SNASFDCEVVPKEPALVILKMTCPPGANAGFELEVSAGMNNATHLSCSSENGTEYRTVE 780
Db 721 SNASFDCEVVPKEPALVILKMTCPPGANAGFELEVSAGMNNATHLSCSSENGTEYRTVE 780
Qy 781 TLANSTSVNITITVSCGKMAAPRNTCTTGTITPPPDGSPNITSVSHSVKXKSGF 840
Db 781 TLANSTSVNITITVSCGKMAAPRNTCTTGTITPPPDGSPNITSVSHSVKXKSGF 840
Qy 841 EASHGPRIKAYAVILTTGEAGHPSADVLKTYDDFKKASDPTVYTLITTEKGSQSISE 900
Db 841 EASHGPRIKAYAVILTTGEAGHPSADVLKTYDDFKKASDPTVYTLITTEKGSQSISE 900
Qy 901 VLKYEIDVGNESSTLGYNGKLEPLGSTRACVAGFTNTTTPHONKGLDGAESYVSERY 960
Db 901 VLKYEIDVGNESSTLGYNGKLEPLGSTRACVAGFTNTTTPHONKGLDGAESYVSERY 960
Qy 961 SDAVSLPODPGVICGAVFGCITFGALVITYVGGFIPWRKKRDANKNEVSFOIIPKSKL 1020
Db 961 SDAVSLPODPGVICGAVFGCITFGALVITYVGGFIPWRKKRDANKNEVSFOIIPKSKL 1020
Qy 1021 IRVENFEAYFKKQADSNCGFAEEYEDLKVIGISQPKYAEIAENRGKRNRYNNVLPYDIS 1080
Db 1021 IRVENFEAYFKKQADSNCGFAEEYEDLKVIGISQPKYAEIAENRGKRNRYNNVLPYDIS 1080
Qy 1081 RYKLSVQCHSTDDYNNAMYPGSHSKOPIATQGPLPNTLKDFFRWMEKKNVVAIIMLTJK 1140
Db 1081 RYKLSVQCHSTDDYNNAMYPGSHSKOPIATQGPLPNTLKDFFRWMEKKNVVAIIMLTJK 1140
Qy 1141 CVEGQRTCEBYWPSKQADYDITVAMTSEIVPEWTIRDFYTKNIQTSSEHPLRQFHF 1200
Db 1141 CVEGQRTCEBYWPSKQADYDITVAMTSEIVPEWTIRDFYTKNIQTSSEHPLRQFHF 1200
Qy 1201 TSWPDHGVPTDITLLINFRYIVRDYMQSPESPILVHCSAGVGTFTFALDRLIYOIE 1260
Db 1201 TSWPDHGVPTDITLLINFRYIVRDYMQSPESPILVHCSAGVGTFTFALDRLIYOIE 1260
Qy 1261 NENIVDVGIVYDRLMRHPLMVOTEDQVFLNQCVDIVRSQKSKVDLIYQNTAMTIY 1320
Db 1261 NENIVDVGIVYDRLMRHPLMVOTEDQVFLNQCVDIVRSQKSKVDLIYQNTAMTIY 1320
Qy 1321 ENLAPVTTFGKTINGYIA 1337
Db 1321 ENLAPVTTFGKTINGYIA 1337

```

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; Sequence 6275, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6275
; LENGTH: 1997
; TYPE: PR
; ORGANISM: Human
US-09-949-016-6275

```

Query Match 17.7%; Score 1242; DB 4; Length 1997;

Best Local Similarity 29.6%; Pred. No. 2.7e-71;

Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

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Qy 123 FDIKAVISSTNVILTKSNDTASERKYVYKHKMENKTTIVVHOPMCNITGLRPATSY 182
Db 759 FDHVEYTIKNNKNIQTKSLP-----KSHNE-----CVFQVLVGRILY 796
Qy 183 VFSITPGIG---NEWGDPRIKIVTEPIPVSDLEVALTGVRKALMSNGNGTSCV 238
Db 797 SVVITTKSGOYEANEQ-GNRTI-----BEVYDILNRKSTEDLHVYSGANG----- 844
Qy 239 LLSISGSH--ELTQDSRL-----QVNI SOLKGVQY-----NINPYLQSNKT 280
Db 845 ---DVDQYEIQLLFNMKVFPPFHLVNTATEYRFTSLTGRQYKILVLTISGVOQSART 901
Qy 281 KG-----DPLG-----TEGGIDANS-----TERRASPPAPYHDESL 313
Db 902 EGFTSVSAVKNHISNKGATDLSLTWNTPGGGVDSVTVSAPRHSQKXDSQTPKGN--- 957
Qy 314 VGPVDPSSGOOSRDTEVLVLGEPGTRYNATVYSQANGETGQPOAIEFRTNALQVFDVT 373
Db 958 -----VFEHTFRLRLEAGRQYQIMLAS--VSSLSKQCNVNGRTVPASVQGYI 1002
Qy 374 ANV-IGATSLTLIMKVSNDNESSNVTYKIHVAGETDSNINVSPPRA-----VITGL 424
Db 1003 ADNAVSSYLIVSWOKAGAVAR--RYDILLTLTENGILLRNTSEPAITTKQHKFEDLTFGK 1059
Qy 425 RSSTFNITVCPVLGDIESTPGFLOVHPVPVSDPRVTVSTTEIGLAMSHDAAESCQM 484
Db 1060 K-----YKIQIILVSGGLFESKEQTEGRYPAAVTLRLITENSIRHLSTRWTASBESLSWY 1115
Qy 485 HI---TOEGAGNSRVEI--TTNOSIIIGLFPGTKYCFEIVPGMGTGASRTVCNRYTP 540
Db 1116 NIFLYNPQDNLQERAOVDPLVQSFQUNLQGRMTKMWIVTH--SGELSNSEFIRGRIVP 1173
Qy 541 SAVFDIHVVYVTTTMMMDKSPDGASEYVYHLVIESKGSNHTSYDAITLQGLIPGT 596
Db 1174 ASVSHLRGSRNNTTUSLWMNSPASGDFD-YELLVYNPNGTKKENMWDKDLTEWRFGGL 1232
Qy 597 IPELTNITISPEVDHWGDPNSTAQYTR-----PSNVSNIDVSTNTTAAITL-----SWQN 647
Db 1233 VPGKRYLMV---VHSGDLSNKVTAESRTAPSPSLMSPADIANATSLATITWKGPDPWTD 1289
Qy 648 FDDASPTT---SYCLIEKAGNSNATQVVDIGITDAITVELIPGSSYVEIFQVGDG 704
Db 1290 YNDFEIQMLPRDALVTFNPNYNNRKEGRIVG-----LAPGRGYQFNVATKVSIDS 1339
Qy 705 IKSL-EPGRKSCCTDPASMASPDECVVPKEPALVILKMTCPPGANAGFELEVSAGMNNAT 763

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RESULT 4

US-09-949-016-6275


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Db 1340 WKTYSKEIFGSRVTRKPKDKIOMLHCR-PONSTAIACSWIPDSDPDGYISIE-----CR 1390
Qy 764 HLESCESENGEYRTEVLYLNF-----STSYNISITTVSCGKMAAPRNTCTGTIDPP 818
Db 1391 KMTIOVEFSRKLKEKESLSLIMMLVPHKRLVSIKQASAGMTSEVEDSTITMIDRPP 1450
Qy 819 PDGSPNI-----TSVSHNSVK--VKFSGFASHGPICAYAVILTTG-----EAGHP 862
Db 1451 P--PPIHVNBEKODLISKSGINFTVNCMSWFDNTGAVKFTVVVREADGDELKPEQHP 1508
Qy 863 SADVLKTYDDFKKASDITYTYLIRTEBKRSQSLSBVLKYEIDVGNSTTLG----- 916
Db 1509 LPSYLERHNASIRVQYTNV--FASKCAENPNSNKS----FNIKLAGEMESLGGKDP 1562
Qy 917 ---YNGKLEPLGSRACVAGFTNITFHPOKGLIDGASVVSFR--YSDA-VSLP--- 967
Db 1563 QQKFCDDPLKPHYRISIRAFIO-----LPD--EDLKEFTKPLSDTFFSLPTT 1611
Qy 968 -ODPGVIGAVFGCIFGALVI---VTVGFIEMRKK--RKDAKNEVSFSQIRP----- 1015
Db 1612 ESEB--LFGAIEGVSAGLPLIGMLVAVALLICQKXSHGERPSALISIRDRPLSVHL 1669
Qy 1016 -----KSKLIRVENFEAYFKQOADSNGFAEYEDLKLVGISQPKYAAELAENRG 1067
Db 1670 NLGQKGNRKTSCKPIKIQFEGHFMKLQADSNYLLSKEYEELKQVGRNOSCDIALPENRG 1729
Qy 1068 KNRNYNVLPRDISVVKLS-VQTHSTDYINANWMPGYHKKDFIATQGPLPNTLKDFPM 1126
Db 1730 KNRNNLPLPDATRKVLSNDDPCSDYINASYIPGNFRREYLVTOGPLGTQDDPM 1789
Qy 1127 VWEKNVAILMLTKVEQGRKCEEYWPSSKO-AQYGDITVAATSEIYLPMTIRDFTVK 1185
Db 1790 VMEGNVNIWVQCVKGRKCDHWMPADODSLYGDLLQMLSESVLPMTIRREKIC 1849
Qy 1186 NIGTESHP--ROFHTSPDHGVPDITDLINFRYLVRDYMKSPSPSLVHCSAGVG 1244
Db 1850 GEEOLDHRLIRHRYHWMPDHGVPEETQSLIQFRTVRDYINRSPGAGPTVHCSAGVG 1909
Qy 1245 RTGFTALIDRLIYOIENENYDVYGIYVLDLHMRPLWQTEDOYVPLNQCTLDIVRSQD 1304
Db 1910 RTGFTALIDRLIQLQDSKSDYIQAHDILHRYHVMVQTECYVYLHQCVRDLARAKL 1969
Qy 1305 SKVDLIYQNTTAMTYENLAP 1325
Db 1970 RS-----EQENPLPIYENVNP 1986

RESULT 5
US-09-949-016-8049
; Sequence 8049, Application us/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8049
; LENGTH: 1903
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8049
Query Match 17.7%; Score 1241, DB 4; Length 1903;

```

```

Best Local Similarity 29.3%; Pred. No. 2,9e-71;
Matches 395; Conservative 198; Mismatches 507; Indels 248; Gaps 54;

Qy 125 IKASISPT-----NVILTKWSNDTFASEYKVVH-----KNEKNTITVHQ 169
Db 646 VQGVSVNSASRSDYLRAKSWHATGDFHYETITKNNFIQTSKIPSENE----- 696
Qy 170 WCNITGLRPATSYVFSITPGIG-----NETWGDPRVIKITEPIIPVSDRLVALTGVRKAL 225
Db 697 -CVFQVLPRGLRYVYVTTTSGQYEANEQ--GNGGTI-----PEVYKULTLNRSTEDLHV 749
Qy 226 SMSNGNSTACRVLLESIGSHE--ELTQDSRL-----QVNISDLKPGVQY---- 268
Db 750 TWSGANG-----DVDQYEIQLLFNDMKVFPFHLVNTATREFTSLTPGRQYKLV 800
Qy 269 -NINPYLQSNKYG-----DPLG-----TEGGLDASN-----TERSR 300
Db 801 LTTISGDVQOQSAFIEGFTVPSAVKNIHISPNCATDLSLVNMTWPGGQDVDSYTVSAFRHSQ 860
Qy 301 AGSPAPVHDSLVGVPDPSGQSRDTEVLLVGLRGTNRNATVYSOAANGTEGQPOAI 360
Db 861 VDSQTIIRK-----VFHTFHLEAGEQYQIMIAS--VSGSLKQNLNV 901
Qy 361 EFRNIAIQVPDYAVN-ISAISLTLIKVSDNESSNYYKIHVAGETDSSNLVSEPR 419
Db 902 VGRTPASVQGVADNAYSSYSLIVSQKAGVAE---RYDILLTEGILLRMTSEBAT 958
Qy 420 -----VIRGLASSFTNYITVCVYLDIGTGFLOVHPRPVPSDFRTVSTTEIG 471
Db 959 TKQHFEDLTPGKK---YKIQILTVSGGLFSKSAQTEGRVPAVVDLRTTENSTRLS 1014
Qy 472 LWSHDAESFQMI---TOEGAGNSRVEI--TTNQSIIIGLFGTKYCFEIVKPGPNT 527
Db 1015 FRMTASEGLSWYIFILNPBGNIQERAOVDPLVQSSFOULGRMYKMWIVH--SGE 1072
Qy 528 EGASRTVCNRTVPSAVPDIDHVVYVTE--WMLDWKSPDGASEYVYHLVIESKHSNHTST 586
Db 1073 LSNESFIFGRTVPAVSGLHRSNNTTDSLWFNMSPASGDPDF--YELLVYNPGTKKENW 1131
Qy 587 YDKAIT---LQGLIRGLNYITISPEVDHVGDNSTAOYR-----PSNNSINDVSTNT 638
Db 1132 KDXDLTEMRFGVLPGKRYVLMV---VTHSGDLSNKYAESRTAPSPSLMSFADIANTS 1188
Qy 639 TAATL-----SWQNDPASPTV---SYCLILEKAGNSSNATGVNDIGITATVTELIPGS 691
Db 1189 LAITWKPDPDWTIDNDELQLPDALTVPFNNKRSSEGIYV-----LRGR 1238
Qy 692 SYTVEIFPAOVGDGKSL--EPGRKSFCTDPASMASPDECVVPKEBALVLMKTCPPGANAGF 750
Db 1239 SYQNVKTVSGDSKMTYSKPIFGSVTRKPKDKIOMLHCR-PONSTAIACSWIPDSDPDGY 1297
Qy 751 ELEVSAGANNATHLBSCSSENGTEYRTEVLYLNF-----STSYNISITTVSCGMAAPT 805
Db 1298 SIE-----CRMDQVEFSRKLKEKESLSLIMMLVPHKRLVSIKQASAGMTSESV 1349
Qy 806 RNTCTGTIDPPRPGSPNI-----TSVSHNSVK--VKFSGFASHGPICAYAVILTTG 857
Db 1350 EDSITTMIDRPPP--PPIHVNBEKODLISKSGINFTVNCMSWFDNTGAVKFTVVVRE 1407
Qy 858 -----EAGHPADVLKTYDDFKKASDITYTYLIRTEBKRSQSLSBVLKYEIDVG 909
Db 1408 DGDDELKPEQHPPLPSYLERHNASIRVQYTNV--FASKCAENPNSNKS----FNIKLG 1461
Qy 910 NESTTLG-----YNGKLEPLGSRACVAGFTNITFHPOKGLIDGASVVSFR-- 959
Db 1462 AEMESLGKCDPTQOKCDDPLKPHYRISIRAFIO-----LPD--EDLKEFTKPL 1510
Qy 960 -YSDA-VSLP---QDPGVIGAVFGCIFGALVI---VTVGFIEMRKK--RKDAKNE 1007
Db 1511 LYSDFPSLPTTTSER--LFGAIEGVSAGLPLIGMLVAVALLICQKXSHGERPSAR 1568
Qy 1008 VFSQIRPKSKL-----IRVENFEAYFKQOADSNGFAEYEDLKLVGISQPKYAA 1060

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Qy 1008 VSPSQIKP-----KSKSLIRVENFEAYFKKQADSNCGPAEYEDLKLVGISQPKYAAELA 1063
Db 1118 -----LPPYLMKRRHPIPIHSFQSYEAKSAHAHQTFQFEBELKVGKQPPLEAHP 1172
Qy 1064 ENRGKKNYNNVLPYDISRVKLSV---QTHSTDYINANNYMGHYSKKQFIATQGPLPNTL 1120
Db 1173 DNIHKNNYHPLPDPHSHRVRLTQLPGEPHS--DYINNFIPIGSHTEIINTQGPLKKTLL 1230
Qy 1121 KDFRMMWKKVVAIIMLTCKVEGQRTKCEYMPSKQAQ-DYGIITYAAMSEIYLPKPTI 1179
Db 1231 EDFRLTWEEQOVHAIIMLTVMEMGRVLCHEHYMPANSTPVTHGHITTHLLAEPEDEWTR 1230
Qy 1180 RDPFVKIKQTSSEHPLQFHTSMQDGVPTDILLNFRLYVADYKMSPPESPIIVHC 1239
Db 1291 REFOLQGTGTEQKQRRVKQLQFTTPDHSVPAPSSLLAFVELVQSVQVATGCKGPIIVHC 1350
Qy 1240 SAGVGRGTGTALDRLIYQIENENTVDYGIYDLMRMRPLMVQTEDOYVELNOCVLD-I 1238
Db 1351 SAGVGRGTGTVALRLRLRLQLEEKVADVFNVTILRLHRLPMIQTLISQYIFLHSCILNKI 1410
Qy 1299 VRSQKDS 1305
Db 1411 LEGPPDS 1417

RESULT 7
US-09-822-871-4
; Sequence 4, Application US/09822871
; Patent No. 6723547
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; FILE REFERENCE: CL001219
; CURRENT APPLICATION NUMBER: US/09/822.871
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2301
; TYPE: PRT
; ORGANISM: Rat
US-09-822-871-4

Query Match 12.3%; Score 864; DB 4; Length 2301;
Best Local Similarity 23.5%; Pred. No. 9.6e-47;
Matches 405; Conservative 216; Mismatches 533; Indels 568; Gaps 77;

Qy 87 GESSGANDS---LTPPEGSGNGTGDASOKTPTSGPSFVFDIKAVSISPTNVIILTW----- 139
Db 647 GESSLSSENDIFVTRTPED-----BPES---SPQ-DVQVTVGPSSELRLKWSPE 691
Qy 140 KSNNTAASEYKVVVKKH---MENEKTIIVVHOPMCNTGLRPAISYVFSTIP-----GIG 191
Db 692 KPCNIIIA-YEVLQNAADTLFVKNTSTDTII-----ISDLKPYTLIYISIRSTRIRLGHG 744
Qy 192 NETGG--DPRVIKYTEPIP--VSDLRVALTGVRKAALSWNGNG--TASCVLLSEISGSH 246
Db 745 NQSSSLSVTSRSEVPSPAPENITYKNISGEIISFLPPRSPNGIICKYITILKRSMSH 804
Qy 247 BELT-QDSRLQVNIISDLKPGVQVINPYLLQSNKTKGDPGLTEGGLDASNTERSRAGSPT 305
Db 805 EARTINTSLTQITGLKKYTHYVIE--VASATLKGE--GIRSRPISILTEEDAPDSPP 859
Qy 306 APVHDESLVG-----PVDP-----SSGOQRNDTEVLV--GLEPGR 340
Db 860 QNFSVVKQSLGVTTWMLSWQPLEPNCIILYTYVYWDKSSLRAINATEASLVSLDLVND 919
Qy 341 YNATVYSQAAANGT-EGQPOAIEFTNAIQV---DYTAVNISATSLTLI----- 386
Db 920 YGACVTASTRGDGNARSSIIINFRTPEGEPSDPNDVHYVNLSSSILTLFTTPVKPNCI 979

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Qy 387 -----KVSNDNESS----- 395
Db 980 IQYISVYTYQNTSGTFVQNFLLQVTKESDNTVYARLYRLAIFSYTFWMLASTSVGN 1039
Qy 396 -----NTYK-----IHVAGETDS-----NLNVEPR 418
Db 1040 KSDI IHVYTDQDIPBGPVGNLTFESISSPTAIHVSMPSPQNGLVFYYSILNLQOSPPR 1099
Qy 419 AVIP-----GLRSTFNITVCPVLGIBETPGF-----LVH-----T 452
Db 1100 HMIPPLVTENSIDPDLEKTYDIFKITP-----STEGKSEITYTQLHKTEDVPT 1154
Qy 453 PVPVSDPRTVTVSTTEIGLAMS---SHDAESFQMHTIIEGAGNSRVEITNQSIIGCL 509
Db 1155 PPI-INTFK--NLSTISILSMDDPLKPNGAIIQHLITLQSPHANHFVTSGNHIVLEEL 1211
Qy 510 PPGTKYCFEIVPKPGNCTEGASRTVCNRYPSAVF---DIHVVYVTTTEWMLDK--SP- 563
Db 1212 SPFLYSPFAARFMKGL--GPSILFFYTDSEADLAPQNLTLINTYSDFWMLTMSPSPL 1270
Qy 564 DGASEYVYHLVIESKSGSNHTSYDOKAIT-----LQGLIPGLNITITPEVDHWGD 616
Db 1271 PGGIYKYSFKI---HEHETDVFYKNIISGLQTDAKLEGEPVSTSVSVAFTKVGNGN 1327
Qy 617 PNS-----TAQYTRPSNVSNID--VSTWTTAATLSMNPQDASPTYSYCL--LIEKAGNS 668
Db 1328 QYSNVVEFTTQESVPEAVRNIECVARDMOSVVM---DPRKTINGIILHMITVGNIS- 1383
Qy 669 NATQVWTDIGITDA--TVTELIPGSSYTVLEIFAQVGDGKISLEBGRKSPCTDPASMASFD 726
Db 1384 -----TKVSPRDTYFTTKLLPNTSYVEFVRASTAG-----EGNEBRC-DISTLP--- 1428
Qy 727 CEVYKPKBALV-----LKTCP----- 743
Db 1429 -ETVPSAPTVNAFNSVOSTSATLWTKEDTIFGYFQNYKITTOLRQAKCREMEPECEIEH 1487
Qy 744 -----PG----- 745
Db 1488 QKDQVLYEANOETETVGLKKFRMYRFOVAASTNVGYSNASEWISTQTLPPRPPGPPENV 1547
Qy 746 ---ANAGELEFVSSGANN-----NATHLESCESENGTEYRTE 779
Db 1548 HVATSPFGINIS---MSBPAVITGPFYLLDVKSVDDDDDNISFLKS--NEENKT---TE 1600
Qy 780 VTYINFTSYNISTIT-----TVSGKKAAPFRNCTTGTITDPP----- 818
Db 1601 INNLEVFTRYSVVITAFVGNVSRAYTDGKSABEVIITLLESVPKDPNNMTFOKIPDEVT 1660
Qy 819 -----PDGSPN-----ITSVSHNSYVKFSGFEASHG- 845
Db 1661 KFQULTPEPSQPNINIRYQALVYREDDPTAVQIHNFSIIQKDTISIIAMLEGLKGHTY 1720
Qy 846 PIKAVAVILLTGEAGHSADVLKTYD-----DPKGAADTYVYVYLIR-- 888
Db 1721 NISVYAI-----NSAGAGPKVQMRITMDIKAPARBSKPIPIRDATGKLVSTITTIMP 1776
Qy 889 -----TEEKGRSQSLSEVLKTEIDVGNES-----TTLGYTN-----GKL 922
Db 1777 ICYVNDHGPRIYNOVLVAETGAQOD--GNVYTKWDAVFNKARPFTYMGFPNPPICEBKT 1835
Qy 923 EPLGSYACVAGFTNIFHPQNK-----GLIDGASEYV-----SFSRYSADV- 964
Db 1836 KFSGNBEIYVIGADNACMIPENEBKICNGPLKPKQYLFKFRATNVMGQPTDSEYSDPIK 1895
Qy 965 -----SLPDPGVICGAVFGCIGALVIYV--VGGEIFMRKKRK-----DAKNEVSF- 1010
Db 1896 TLGGLSERTVEIILSVTLICLISLILGTALFAFVRIHQKKBEGTYSPPRAEIIIDTFK 1955
Qy 1011 -----SQIKPKSKLIRV-----ENFEAYFKKQADSNCGPAEYEDLKLV 1051
Db 1956 LDOLITVADDELKDERLRLLSYRKSIKPISKSKSFLQVHELCTNSMLKFOEBSSEL--- 2012

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: PRIOR APPLICATION NUMBER: 60/241,755
:
: PRIOR FILING DATE: 2000-10-20
:
: PRIOR APPLICATION NUMBER: 60/237,768
:
: PRIOR FILING DATE: 2000-10-03
:
: PRIOR APPLICATION NUMBER: 60/231,498
:
: PRIOR FILING DATE: 2000-09-08
:
: NUMBER OF SEQ ID NOS: 207012
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 8051
:
: LENGTH: 1246
:
: TYPE: PRT
:
: ORGANISM: Human
:
: US-09-949-016-8051

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	Query Match	12.1%	Score 854;	DB 4;	Length 1246;
	Best Local Similarity	28.0%	Pred. No. 1,7e+46;		
	Matches 279;	Conservative 158;	Mismatches 347;	Indels 212;	Gaps 41;
Qy	452	TPWPVS-----DFRVTVSTTEIGLAWSHD-----ESPOMHTOEGAGNSREVT	499		
Db	329	TPPEISGNISSGMPDFNSDYEETTSQPYMPOSASAPESBDFVSLPMEYENNTLSSET	388		
Qy	500	TNOSIIIGLPGTKYCFEIPKPGNGEGASRTVCNNTVSAVDIHV-----	548		
Db	389	EKSTSGSFPPVQWILTWLPKPEPTADG-----PHIEREENFTEYLM	434		
Qy	549	VYVTTTMMMLWMSKSPDGASEYVYHLVLIKSGSNHSTYDKATILQGLIPTLYNTTISP	608		
Db	435	VDEAHFVVALKEP-----GKKYKSLVTTTSSSGSCSTRSGSKSL-----SFYISP	482		
Qy	609	EVDHWGDPNSTAQTTPRSANSNIDVSTNTTAAITSM-----ONFPDASPTYSCLLEKA	664		
Db	483	SGE--WIEBELT-----EKPOHVS--VHVLSSIT--ALMSWTSOENNVSTIVS-VSLTCKQ	533		
Qy	665	GNSGN-ATQVATDIDGATVATTELPGSSYTWIEPAQVGGDKSLPEPKSFCTDPASMA	723		
Db	534	KESQBLEQYCTQVNSSKPIIENLVFGAQOYVILKRGPLI-----GPPS--DPVTFA	585		
Qy	724	SF-----DCEVVPKP-ALVILKTCP--PGANAGFELEVSSGAMNATHLESCESSNGTEY	776		
Db	586	IVPTGIKIDLMYPLGPPTAVVLSMTPEPYGVPRKYVEMF--YFNPAT--MTSEWTTY	639		
Qy	777	RTEVLYNFTS-----VNISTTYS CGMAAPNTNCTTG-----ITDPEPPDG	821		
Db	640	EIAAT-VSLTASVARIANILPAMYINFRMTWTWGG--PEUSCCDSSTISFTIAYV---	691		
Qy	822	SPNTTSVSHNSVKYKFS-----GPEAGHCPKAKAVI-----LTGEGAGH	861		
Db	692	APETTSVEYFNLSLIYSWTYGGDDTTDLSHSMILHMVVAEGKKIKKSVTNVMTAILSL	751		
Qy	862	PSADVLTYYDFKKGASDYTYTYLIRP-----	890		
Db	752	PPGDIYMLSVTACTERGSGNTSMLRLVYKLEPAPKSLFAVNKTQTSVTLHWEEGVADFE	811		
Qy	891	-----EKGSQSLSEVLKYEIDVGNESTLTGYNGCLPELGSYRACVAGFTVTFHPQKG	946		
Db	812	VFCQVSSQTK--LQEPVAVSHVYI-----SSLPATAYNCVTSFSH-----	856		
Qy	947	LIDGASVYSFSRYSDAVSLPQDPGVICAGVFCIGALVITVYGGFIEMRK-----RK	1001		
Db	857	---DSPSPVPTFIAVSTWYI--EMNPRVAVVISVLAISTLLIGLLVTLILIRKHLQAMRE	912		
Qy	1002	DAKNNEVSFSGIKP-----KKSXL-----IRVENFAVYKKQAOASNGCFAREY	1044		
Db	913	CGAGTFVNFASLERDQKLPYMSKNGKLKRRKLTNPFQVLDDBPAYIKDMAKOSDYFSLQF	972		
Qy	1046	EDLKLVGISQRYAAELAENRGKRNYYNVLPYDISRYKL--SVQTHSTDDYINANTPGYH	1104		
Db	973	ELKTLIGDIDHPADLPLNRCKNRKYTILPYDFSRYVLVSNBEBGADYINANYIPGIN	1033		
Qy	1105	SKQPIAIAQSGPLNTLKDFPMKMEKANYAIIIMLTLCYEOGRTKCEEYWP--SKAODYD	1166		
Db	1033	SPOEIAIAQSGPLNTRNDPMKRVVLAQKSKQIIIVMLTQCKEKRKVKCDHWHPTFEEPIA	1092		

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QY 1164 TTVAATSEIHLBEWIRPTVGNIGTSESHRLQCHFTSMRPHGV--DTTDLINPRL 1221
Db 1093 ITVEIISSEEDODMACRHRLIN--YADEQODVMHNYNTAMPHGVPTAAAESILDFVHM 1150
QY 1222 VRDVKOSPPESPILVHCSAGVGRGTFTALDRLLFYOLENENVTVDVGYLDLRMRPLM 1281
Db 1151 VRQQAATKS--KSPMIHCSAGVGRGTFTALDRLLQHTIHDEHFDVILGLVSEKRSYRSM 1208
QY 1282 VQTEBOYVFLNQCV--LDIVRSQKSKYDLLIYQNTT 1315
Db 1209 VQTEBOYTFIHQCVQDMMKKKQDCISIVYEENS 1244

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RESULT 10
US-09-949-016-8052
; Sequence 8052, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8052
; LENGTH: 1246
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8052

```

```

Query Match 12.1%; Score 854; DB 4; Length 1246;
Best Local Similarity 28.0%; Pred. No. 1.7e-46;
Matches 279; Conservative 158; Mismatches 347; Indels 212; Gaps 41;

Db 452 TPVAVS-----DFRVVSTTEIGLAWSHDA-----ESFOMHITGAGNSREIIT 499
||:|
||:|
Db 329 TPEISGNISGMPFNSSDYETTSQPYWMDASAPASEDEVSVLPRHEYNNTSLSET 368
||:|
||:|
Db 500 TNOSIIIGLPPGYKCFEIVPKGNGTEGASRTVCNRTPSAVIDHV----- 548
:|
:|
Db 389 EKSTGSGSFEPVQIMLTLPKPKPTAFDG-----FHIHERENPTEYLM 434
:|
:|
Db 549 VYVTTTMMIDMKSPDGASeVYVYHVLIESKHGNSHTYDKAITLQGLPGLYNTTISP 608
||:|
||:|
Db 435 VDEAHEVAELKEP---GKYLDSTYTTSSSGSCETRKSSQSAKSL-----SYIISP 482
||:|
||:|
Db 609 EVDHAGDPNSTAQYTRPSNVSNIDVSTTTATATLSW---ONFDDASEPTYCYLIEKA 664
||:|
||:|
Db 483 SGE--WIELT---EKPOHVS--VAVLSTT--ALMSWTSQGEYNNTIYSV--VSLRCQKQ 533
||:|
||:|
Db 665 GNSNS-AIQVVTDIGITDATYTELIPGSSYTYEIRAQVDDGIKSLPEGRKSFCTDPASMA 723
||:|
||:|
Db 534 KESQRLERQCYCTQVWNSKRIENLIVPAQOYQVVIYLRKPLI-----GPPS---DVTFA 585
||:|
||:|
Db 724 SF-----DCEVVPKRP-ALVYKTCP--PGANAGFELEVSAGAMNNATHLSCGSENGTEX 776
||:|
||:|
Db 586 IVPGICIKDMLTYPGLPFLVAVLSWTPPYGVCPKRYVEMF--YFNPAI---MTSEWTTY 639
||:|
||:|
Db 777 RTEVYLYNFSTs-----YNISITVYSGKMAAFTRYCTTG---ITDPEPPDG 821
||:|
||:|
Db 640 EIAAT-VSLTASVRIANLLPAMYVNFRAVMTVMTGD---PELSCDBSSTISFIAFV---- 691
||:|
||:|
Db 822 SPNTTSVHNSVYKAFS-----GPEASHGPIKAYAVT-----LTGEAGH 861
||:|
||:|

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Db      692 APEITSEVEFNSLLYSMTYGGDTTDLSSRLMHWVAEGKKIKKSVTRNMTAILSL 751
Qy      862 PSADVLTYYDDPKGASDTYYTYLIRTE----- 890
Db      752 PRODIINLSVTACTEGSNTSMRLVLEBPAPPKSLFANVKTQTSYTLTLMVEGVADFFE 811
Qy      891 ----EKGRSOSLSEVLKYEIDVGNESSTLGYNGKLEPLGSYRACVAGFTNTTFHPONKG 946
Db      812 VFCQGVSSQKTK--LQEPVAVSSHVVTI-----SLLPRAVNCSTSPSH----- 856
Qy      947 LIDGASVYFSGRYGNASVLPDOPGICAGVFCIGALVITYVGGFTFMRK-----RK 1001
Db      857 ---DSPVPTFTAVSTMTV--EMNPVNVISVALISTLLIGLLVTLILIRKGLQMARE 912
Qy      1002 DAKNNEVSFSQIKP-----KSKL---IRVNFPAVFKQOADSNGFAEY 1045
Db      913 CGAGTFVNFASLEBROGKLPYNNKNGKRLTNVQDDPDAYIKDMAKSDYFSLQF 972
Qy      1046 EDLKVGISQPKYAELAEENRGKRNRYNVLPYDISRVKL-SVQTHSTDDYINANYMPGYH 1104
Db      973 EELKILIGLDIPHPADLPINRCNRYTNILPYDFSRVRLVSNMEEGADYINANYIPGN 1032
Qy      1105 SKDPIATOGPLPNTLKDFRWVMEKNVYAILMLTKVCEOGRTKEEYWP-SKQADYGD 1163
Db      1033 SPOEYIATOGPLPBTNRDPMKAVLQOKSOLIVMLTQCNEKRRVKCDHYMPTEEPYAGD 1092
Qy      1164 ITVANTSEIPLPEWTRIRDTVKNIQTSSEHPLROFHTSMPDHGP--DTTDLILNFRYL 1221
Db      1093 ITVEMISEBQDDMACRHRLN--YADEMODVMHNTYAMPDHGVPPTANAESILQFVHM 1150
Qy      1222 VDDYMKOSPESPILVHCSAGVGRGTFTALDRLLYQIENENTVDYGIYVDMRMRPLM 1281
Db      1151 VROQATKS--KGPMTIHCSAGVGRGTFTALDRLLQHRDHEFVDILGLVSEMSYRMSM 1208
Qy      1282 VQTEDOYVFLNQC--LDIVRSQKSKVDLIYQNTT 1315
Db      1209 VQTEQYIFIHQCVOQMMMKKQOFCISDIYENVS 1244

RESULT 11
US-09-949-016-8053
; Sequence 8053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMOBPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8053
; LENGTH: 1246
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8053

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Query Match 12.1%; Score 854; DB 4; Length 1246;
 Best Local Similarity 28.0%; Pred. No. 1.7e-46;
 Matches 279; Conservative 158; Mismatches 347; Indels 212; Gaps 41;

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Qy      452 TTPVPVVS-----DFRVTVSTTEIGLAWSSHDA-----ESFQMTITGAGNSRVEIT 499
Db      329 TPEIPSGNISGWDPMNSDYEITTSQPYWMDASABESBDEFVSLPMEYENNSTLSET 388
Qy      500 TNGSIIIGLFPGRTKCFEIVPKGPNGTGASRTVCNRTVSAVFDIHV----- 548

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Db      389 EKSTSGSFFFPVGMILTWLPPKPTAFDG-----FHHIEREENFTYIM 434
Qy      549 VYTTTEMLDMWKSPDGAASEVYHLVIESKGSNHTSTYDKAITLQGLPGLTNYITISP 608
Db      435 VDEEAHEFVALKEBP---GKYKLSVTTFSSSGSCETAKSASKL-----SFYISP 482
Qy      609 EVDHVMGDPNSTAQTSPSNVSNIDVSTNTAATLSM-----QNRDDASPTYSYLLIEKA 664
Db      483 SGE--WIEBELT---EKPOHVS--VHVLSTT--ALMSWTSOENNSTIVSV-VSLTCQKQ 533
Qy      665 GNSSN-AQVNTDIGITADATVTELLIPGSSTVEIFAQVNGIKSLBGRKSFCTDPASMA 723
Db      534 KESGRLEKQCYCTQYNSKPIIENLVPGAQVQVYILAKGLI-----GPPS---DPVTPA 565
Qy      724 SF-----DCEVYKEP--ALVLTCTP--PGANAGEFELEVSSGAMNATHLESCESENGTEY 776
Db      586 IVPGRIDMLYPLGPPAVVLSWTRPYLGVRKVVEMF--YFNPAT---MTSEWTTY 639
Qy      777 RTEVLYLNFS-----YNISITVSGKMAAPTRNTCTG---ITDPPPDG 821
Db      640 EIAAT-VSLTASVRIANLPAWYNERVNTWGD--PELSCDSSTISFITAPV--- 691
Qy      822 SPNITSVSHNSVKVKS-----GFEASHGPIRAYAVI-----LTGEGAGH 861
Db      692 APEITSEVEFNSLLYSMTYGGDTTDLSSRLMHWVAEGKKIKKSVTRNMTAILSL 751
Qy      862 PSADVLTYYDDPKGASDTYYTYLIRTE----- 890
Db      752 PRODIINLSVTACTEGSNTSMRLVLEBPAPPKSLFANVKTQTSYTLTLMVEGVADFFE 811
Qy      891 ----EKGRSOSLSEVLKYEIDVGNESSTLGYNGKLEPLGSYRACVAGFTNTTFHPONKG 946
Db      812 VFCQGVSSQKTK--LQEPVAVSSHVVTI-----SLLPRAVNCSTSPSH----- 856
Qy      947 LIDGASVYFSGRYGNASVLPDOPGICAGVFCIGALVITYVGGFTFMRK-----RK 1001
Db      857 ---DSPVPTFTAVSTMTV--EMNPVNVISVALISTLLIGLLVTLILIRKGLQMARE 912
Qy      1002 DAKNNEVSFSQIKP-----KSKL---IRVNFPAVFKQOADSNGFAEY 1045
Db      913 CGAGTFVNFASLEBROGKLPYNNKNGKRLTNVQDDPDAYIKDMAKSDYFSLQF 972
Qy      1046 EDLKVGISQPKYAELAEENRGKRNRYNVLPYDISRVKL-SVQTHSTDDYINANYMPGYH 1104
Db      973 EELKILIGLDIPHPADLPINRCNRYTNILPYDFSRVRLVSNMEEGADYINANYIPGN 1032
Qy      1105 SKDPIATOGPLPNTLKDFRWVMEKNVYAILMLTKVCEOGRTKEEYWP-SKQADYGD 1163
Db      1033 SPOEYIATOGPLPBTNRDPMKAVLQOKSOLIVMLTQCNEKRRVKCDHYMPTEEPYAGD 1092
Qy      1164 ITVANTSEIPLPEWTRIRDTVKNIQTSSEHPLROFHTSMPDHGP--DTTDLILNFRYL 1221
Db      1093 ITVEMISEBQDDMACRHRLN--YADEMODVMHNTYAMPDHGVPPTANAESILQFVHM 1150
Qy      1222 VDDYMKOSPESPILVHCSAGVGRGTFTALDRLLYQIENENTVDYGIYVDMRMRPLM 1281
Db      1151 VROQATKS--KGPMTIHCSAGVGRGTFTALDRLLQHRDHEFVDILGLVSEMSYRMSM 1208
Qy      1282 VQTEDOYVFLNQC--LDIVRSQKSKVDLIYQNTT 1315
Db      1209 VQTEQYIFIHQCVOQMMMKKQOFCISDIYENVS 1244

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RESULT 12
 US-09-949-016-8054
 ; Sequence 8054, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMOBPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:57:57 ; Search time 168 Seconds
(without alignments)
2654.891 Million cell updates/sec

Title: US-09-516-728a-4

Perfect score: 7030
Sequence: 1 MKPAREARLPKPSGRLMA.....TIYENLAPVTTPKTINGYIA 1337

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 1428581 seqs, 33359853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7030	100.0	1337	15 US-10-366-547-42	Sequence 42, Appli
2	7030	100.0	1337	16 US-10-723-606-2	Sequence 2, Appli
3	6950	98.9	1337	15 US-10-366-547-44	Sequence 44, Appli
4	6824	97.1	1337	14 US-10-350-501-2	Sequence 2, Appli
5	4508.5	64.1	1238	15 US-10-366-547-47	Sequence 47, Appli
6	4499.5	64.0	1216	15 US-10-366-547-49	Sequence 49, Appli
7	1811	25.8	341	16 US-10-723-606-3	Sequence 3, Appli
8	1242	17.7	1997	15 US-10-634-027-2	Sequence 2, Appli
9	1241	17.7	1997	10 US-09-909-567B-54	Sequence 54, Appli
10	1241	17.7	1997	16 US-10-408-765A-2135	Sequence 2135, Ap
11	1241	17.7	1997	16 US-10-497-692-4	Sequence 4, Appli
12	1230	17.5	1450	16 US-10-497-692-14	Sequence 14, Appli
13	1130	16.1	1118	14 US-10-245-539-2	Sequence 2, Appli

14	1130	16.1	1118	14 US-10-245-539-8	Sequence 8, Appli
15	1127	16.0	1093	14 US-10-245-539-4	Sequence 4, Appli
16	969	13.8	1767	15 US-10-087-684-40	Sequence 40, Appli
17	969	13.8	1767	15 US-10-218-779-40	Sequence 40, Appli
18	954	13.6	1767	15 US-10-087-684-41	Sequence 41, Appli
19	954	13.6	1767	15 US-10-218-779-41	Sequence 41, Appli
20	924.5	13.2	1447	16 US-10-497-692-13	Sequence 13, Appli
21	889.5	12.7	336	15 US-10-634-027-4	Sequence 4, Appli
22	879	12.5	1912	17 US-10-772-636-64	Sequence 64, Appli
23	878.5	12.5	312	15 US-10-634-027-6	Sequence 6, Appli
24	878.5	12.5	319	15 US-10-634-027-7	Sequence 7, Appli
25	864	12.3	2301	10 US-09-822-871-4	Sequence 4, Appli
26	864	12.3	2301	15 US-10-673-885-4	Sequence 4, Appli
27	864	12.3	2302	15 US-10-087-684-37	Sequence 37, Appli
28	864	12.3	2302	15 US-10-218-779-37	Sequence 37, Appli
29	854	12.1	1188	15 US-10-331-996A-79	Sequence 79, Appli
30	854	12.1	1188	16 US-10-789-241-34	Sequence 34, Appli
31	831.5	11.8	2281	15 US-10-087-684-6	Sequence 6, Appli
32	831.5	11.8	2281	15 US-10-218-779-6	Sequence 6, Appli
33	827	11.8	2299	15 US-10-466-759-2	Sequence 2, Appli
34	826	11.7	2291	10 US-09-822-871-2	Sequence 2, Appli
35	826	11.7	2291	15 US-10-673-885-2	Sequence 2, Appli
36	826	11.7	2300	15 US-10-087-684-10	Sequence 10, Appli
37	826	11.7	2300	15 US-10-218-779-10	Sequence 10, Appli
38	817	11.6	1367	15 US-10-369-493-5508	Sequence 5508, Ap
39	817	11.6	1367	15 US-10-369-493-5509	Sequence 5509, Ap
40	799	11.4	1948	9 US-09-808-602-55	Sequence 55, Appli
41	799	11.4	1948	10 US-09-800-198-45	Sequence 45, Appli
42	792.5	11.3	1897	17 US-10-482-029-52	Sequence 52, Appli
43	788.5	11.2	1907	15 US-10-291-265-250	Sequence 250, App
44	782	11.1	310	9 US-09-788-626-15	Sequence 15, Appli
45	778.5	11.1	1502	9 US-09-808-602-54	Sequence 54, Appli

ALIGNMENTS

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RESULT 1
US-10-366-547-42
; Sequence 42, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366,547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-547-42
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Query Match	100.0%	Score 7030;	DB 15;	Length 1337;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1337;	Conservative 0;	Mismatches 0;	Gaps 0;	
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DB	1	MKPAREARLPKPSGRLMALPLLLLRLLGQIIICAGTSPSPIDPSVATVATGNGTQ	60	
QY	61	ISSTAESPHKONGCTPOVETNTSEDGSSGANDSLRTPGCSNGTDCASQKTSSTPS	120	
DB	61	ISSTAESPHKONGCTPOVETNTSEDGSSGANDSLRTPGCSNGTDCASQKTSSTPS	120	
QY	121	PVPDIKAVSIPFTVILTWKSNDRPAASRYKTVVGHKNEKTIIVVHQPNCNITGLRPA	180	
DB	121	PVPDIKAVSIPFTVILTWKSNDRPAASRYKTVVGHKNEKTIIVVHQPNCNITGLRPA	180	

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QY 181 SYFESITPGIGNETWGPRIYKITEPIPVSDLRVALTGVRAKALSWNGNGTASGRVLL 240
DB 181 SYFESITPGIGNETWGPRIYKITEPIPVSDLRVALTGVRAKALSWNGNGTASGRVLL 240
QY 241 ESIGSHEELTODSRLQVNI SDLKPGVQVNIINPYLQSNKTKGDPGLTEGGLDASNTERSR 300
DB 241 ESIGSHEELTODSRLQVNI SDLKPGVQVNIINPYLQSNKTKGDPGLTEGGLDASNTERSR 300
QY 301 AGSPPTAPVHDESLVGVDPSSGQOSRDTEVLVGLPEGTRINATVYSQANGETEGQPQAI 360
DB 301 AGSPPTAPVHDESLVGVDPSSGQOSRDTEVLVGLPEGTRINATVYSQANGETEGQPQAI 360
QY 361 EFRTNALQVFDVAVANISATSLTLIMKVSNDNESSNYTKIHVAGETSDSNLVSEPRAY 420
DB 361 EFRTNALQVFDVAVANISATSLTLIMKVSNDNESSNYTKIHVAGETSDSNLVSEPRAY 420
QY 421 IPELRSTYNTVTCVPLGDIESTPGFLQVHTPPVPVSDFRVTVSTTEIGLAWSHDAE 480
DB 421 IPELRSTYNTVTCVPLGDIESTPGFLQVHTPPVPVSDFRVTVSTTEIGLAWSHDAE 480
QY 481 SFQMHITQGAAGNSRVEITTNOSIIIGLFPQTKYCFEIVPGPMTGEGASRTVCNRTVP 540
DB 481 SFQMHITQGAAGNSRVEITTNOSIIIGLFPQTKYCFEIVPGPMTGEGASRTVCNRTVP 540
QY 541 SAVFDIHVVYVTTTMMWLDKMSPDGASEVYVHLVIESKHGSHNTSTYDKALITLQGLIPGT 600
DB 541 SAVFDIHVVYVTTTMMWLDKMSPDGASEVYVHLVIESKHGSHNTSTYDKALITLQGLIPGT 600
QY 601 LYNITISPEVDHVMGDPNSTAOYTRPSNVSNIDVSTNTTAATLSQONDDASPTYSYCLL 660
DB 601 LYNITISPEVDHVMGDPNSTAOYTRPSNVSNIDVSTNTTAATLSQONDDASPTYSYCLL 660
QY 661 IEKAGNSSNATQVMTDITGTDATVTELLPGSSYVTEIFAQVGDGKSLPEPKSKCTDPA 720
DB 661 IEKAGNSSNATQVMTDITGTDATVTELLPGSSYVTEIFAQVGDGKSLPEPKSKCTDPA 720
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DB 721 SMASDCEVVPKEPRLVLTWCPCPGANAGFELEVSSGAMNNATHLESSESNGETEYRTREV 780
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QY 841 EASHGPIKAYAVIILTTGAGHPADVLKTYDDPFKKGASDTYVYLLIRTEEKGRSQSLSE 900
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QY 901 VLKKEIDVGNESSTLGYNGKLEPLGSRACVAGFTNITTHPQNGKIDGASVYSFSRY 960
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QY 1081 RVKLSVQHSITDDIYNANVMPGYSKODFIATOGPLNLTLDFFRMWENKRYVAIIMLTJK 1140
DB 1081 RVKLSVQHSITDDIYNANVMPGYSKODFIATOGPLNLTLDFFRMWENKRYVAIIMLTJK 1140
QY 1141 CVEQGRKCEBYWPSKQADYDGIITVAMTSEIIVPEWTIRDFYKNIQTSSEHPLRQFHF 1200
DB 1141 CVEQGRKCEBYWPSKQADYDGIITVAMTSEIIVPEWTIRDFYKNIQTSSEHPLRQFHF 1200
QY 1201 TSWPDHGVPTDTLLINFRYLVADYKQSPESPILVHCSAGVGRGTFTIADRLIYQIE 1260
DB 1201 TSWPDHGVPTDTLLINFRYLVADYKQSPESPILVHCSAGVGRGTFTIADRLIYQIE 1260

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QY 1261 NENTVDVGIYYDLMRHEPLAVQTEBDQVFLNQCULDIVRSQKSKVDLIYONTTAMTIY 1320
DB 1261 NENTVDVGIYYDLMRHEPLAVQTEBDQVFLNQCULDIVRSQKSKVDLIYONTTAMTIY 1320
QY 1321 ENLAPVTFGKTNGYIA 1337
DB 1321 ENLAPVTFGKTNGYIA 1337

RESULT 2
US-10-723-606-2
; Sequence 2, Application US/10723606
; Publication No. US20040161821A1
; GENERAL INFORMATION:
; APPLICANT: Falka-Hambjlin, Helena L.
; TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS
; FILE REFERENCE: 200125 447
; CURRENT APPLICATION NUMBER: US/10/723,606
; CURRENT FILING DATE: 2003-11-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-606-2

Query Match 100.0%; Score 7030; DB 16; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKPAAERARLPSPSPGIRWMLPLILLRLGQILCAGTSPPIPDPSVATVATGENGITTQ 60
QY 61 ISSTASFEHKQNGTGPQVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSTGTS 120
DB 61 ISSTASFEHKQNGTGPQVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSTGTS 120
QY 121 PVFDIKAVSISPNTVILLTWKSNDDTAASEYKYVYKHMENKETTIVVHQPNCNITGRPAT 180
DB 121 PVFDIKAVSISPNTVILLTWKSNDDTAASEYKYVYKHMENKETTIVVHQPNCNITGRPAT 180
QY 181 SYFESITPGIGNETWGPRIYKITEPIPVSDLRVALTGVRAKALSWNGNGTASGRVLL 240
DB 181 SYFESITPGIGNETWGPRIYKITEPIPVSDLRVALTGVRAKALSWNGNGTASGRVLL 240
QY 241 ESIGSHEELTODSRLQVNI SDLKPGVQVNIINPYLQSNKTKGDPGLTEGGLDASNTERSR 300
DB 241 ESIGSHEELTODSRLQVNI SDLKPGVQVNIINPYLQSNKTKGDPGLTEGGLDASNTERSR 300
QY 301 AGSPPTAPVHDESLVGVDPSSGQOSRDTEVLVGLPEGTRINATVYSQANGETEGQPQAI 360
DB 301 AGSPPTAPVHDESLVGVDPSSGQOSRDTEVLVGLPEGTRINATVYSQANGETEGQPQAI 360
QY 361 EFRTNALQVFDVAVANISATSLTLIMKVSNDNESSNYTKIHVAGETSDSNLVSEPRAY 420
DB 361 EFRTNALQVFDVAVANISATSLTLIMKVSNDNESSNYTKIHVAGETSDSNLVSEPRAY 420
QY 421 IPELRSTYNTVTCVPLGDIESTPGFLQVHTPPVPVSDFRVTVSTTEIGLAWSHDAE 480
DB 421 IPELRSTYNTVTCVPLGDIESTPGFLQVHTPPVPVSDFRVTVSTTEIGLAWSHDAE 480
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DB 481 SFQMHITQGAAGNSRVEITTNOSIIIGLFPQTKYCFEIVPGPMTGEGASRTVCNRTVP 540
QY 541 SAVFDIHVVYVTTTMMWLDKMSPDGASEVYVHLVIESKHGSHNTSTYDKALITLQGLIPGT 600
DB 541 SAVFDIHVVYVTTTMMWLDKMSPDGASEVYVHLVIESKHGSHNTSTYDKALITLQGLIPGT 600

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Best Local Similarity	99.1%	Pred. No. 0;		
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DB 1 MKPARREARLPERSBGRMALPLLLLLRLGQILCAGGTSPRPDPSPVATVAGENGTO	60			
QY 61 ISSTAESHKONGGTPOVETNTSEDESSGANDSLRTPEGSGNGTGAASQKTPSSGTPS	120			
DB 61 ISSTAESHKONGGTPOVETNTSEDESSGANDSLRTPEGSGNGTGAASQKTPSSGTPS	120			
QY 121 PVFDIKAVSISPTNVILLTWKSNBDTASBYKKTVVGHKMEKTTITVHQPCNITGLRPAT	180			
DB 121 PVFDIKAVSISPTNVILLTWKSNBDTASBYKKTVVGHKMEKTTITVHQPCNITGLRPAT	180			
QY 181 SYVSISIPGIGNEWTGDPVTKVLTETPVPUSDLEVALTGAKKALSMNSNGTASCRLT	240			
DB 181 SYVSISIPGIGNEWTGDPVTKVLTETPVPUSDLEVALTGAKKALSMNSNGTASCRLT	240			
QY 241 ESISGHEELTQDSRLQVNI SDLKEGYOVNINIPYLLQSNKTKGDLGTEGGDAANTERSR	300			
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DB 301 AGSPTPAPVHDESLVGPDPSSGGQSDRTVELVGLBEGTRYNATVYQAANGTEGQPOAI	360			
QY 361 EFRFNALQVPRVATVNI SATSLTLIMKVSNDNESSNTTKIHVAGETDSSLTANSEBRV	420			
DB 361 EFRFNALQVPRVATVNI SATSLTLIMKVSNDNESSNTTKIHVAGETDSSLTANSEBRV	420			
QY 421 IPGARSTFVNIITVCPVLGDI BGTGFLQVNTVPVPSDFRVTWSTTEIGLASSHDAE	480			
DB 421 IPGARSTFVNIITVCPVLGDI BGTGFLQVNTVPVPSDFRVTWSTTEIGLASSHDAE	480			
QY 481 SFQNHITQBGAGNSRVEITTNOSIIGLFPRTKYCFEIVKGBNGTEGASRTVCNRTVP	540			
DB 481 SFQNHITQBGAGNSRVEITTNOSIIGLFPRTKYCFEIVKGBNGTEGASRTVCNRTVP	540			
QY 541 SAVPDIVHYVYTTTMMMLDMKSPGASBYVYHLVIESKHSNHTSTYDKAITLLOGLPGT	600			
DB 541 SAVPDIVHYVYTTTMMMLDMKSPGASBYVYHLVIESKHSNHTSTYDKAITLLOGLPGT	600			
QY 601 LYNITISPEVDHWGDDNSTAQTQYRPNVNSIDVSTMTTAAATLSMOWPDASPTYSCLL	660			
DB 601 LYNITISPEVDHWGDDNSTAQTQYRPNVNSIDVSTMTTAAATLSMOWPDASPTYSCLL	660			
QY 661 IEKAGNSSNATQVVTDITGIDATVTELLPGSSYVVEIFAQVGDGSIKSLPERKSFCTDPA	720			
DB 661 IEKAGNSSNATQVVTDITGIDATVTELLPGSSYVVEIFAQVGDGSIKSLPERKSFCTDPA	720			
QY 721 SMASFDCEVVPKEPALVILKMTCPPGANAGFELEVSSGAMNNATHESSCSSENGTEBYTEV	780			
DB 721 SMASFDCEVVPKEPALVILKMTCPPGANAGFELEVSSGAMNNATHESSCSSENGTEBYTEV	780			
QY 781 TYLNPFSVSYNISIITVSCGRKAAATPRNTCTTGITDPPPOSPIITSVSHNSVYVKSGF	840			
DB 781 TYLNPFSVSYNISIITVSCGRKAAATPRNTCTTGITDPPPOSPIITSVSHNSVYVKSGF	840			
QY 841 EASHGPTIKAVVILITTEBAGHPASADVILKYTDVDPKKASDPVYVYLLIRTEKSGSQSLSE	900			
DB 841 EASHGPTIKAVVILITTEBAGHPASADVILKYTDVDPKKASDPVYVYLLIRTEKSGSQSLSE	900			
QY 901 VLKTEIDVGNESSTLGLSYNGKLEPLGSYRACVAGFTNITTHPONKGLIDGAEYSVFSRY	960			
DB 901 VLKTEIDVGNESSTLGLSYNGKLEPLGSYRACVAGFTNITTHPONKGLIDGAEYSVFSRY	960			
QY 961 SDASVSLQDDPCVTCGAVFGCIPGALVIVTGGFIFMKKKKDKADANNVSPQIKPKKSKL	1020			
DB 961 SDASVSLQDDPCVTCGAVFGCIPGALVIVTGGFIFMKKKKDKADANNVSPQIKPKKSKL	1020			

QY 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPRYAAELAEENKRNYYNVL.PYDIS 1080
Db 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPRYAAELAEENKRNYYNVL.PYDIS 1080
QY 1081 RVLASVQTHSTDDYINANWMPGHSKKDPFATQGP.LPNTL.KDFWVMEKKNYVAILMLTK 1140
Db 1081 RVLASVQTHSTDDYINANWMPGHSKKDPFATQGP.LPNTL.KDFWVMEKKNYVAILMLTK 1140
QY 1141 CVEQGRKCEEWPSKQADYGDITVAMTSEIYLPMTIRDFVKNQIOTSESHPLRQFHF 1200
Db 1141 CVEQGRKCEEWPSKQADYGDITVAMTSEIYLPMTIRDFVKNQIOTSESHPLRQFHF 1200
QY 1201 TSWPDHGVPTDILLINFRYLVADYKQSPSPSPILVHCSAGVGTGTFIALDRILYQIE 1260
Db 1201 TSWPDHGVPTDILLINFRYLVADYKQSPSPSPILVHCSAGVGTGTFIALDRILYQIE 1260
QY 1261 NENTVAVGIVYDLRMRHPLMOTEDQYVFLNQCVDIVRSQKDSKVDLIYONTAMTY 1320
Db 1261 NENTVAVGIVYDLRMRHPLMOTEDQYVFLNQCVDIVRSQKDSKVDLIYONTAMTY 1320
QY 1321 ENLAPVTFGKNGYIA 1337
Db 1321 ENLAPVTFGKNGYIA 1337
RESULT 4
US-10-390-501-2
; Sequence 2, Application US/10390501
; Publication No. US20030148491A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
; PHOSPHATASES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Seed IP Law Group PLLC
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/390,501
; FILING DATE: 13-Mar-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 200125.402C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: 1linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-390-501-2
Query Match 97.1%; Score 6824; DB 14; Length 1337;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;
QY 1 MKPAREARLPSPRSGRLMALPLLLLLRLGQIILCAGTSPSPIDPSAVATATGSENGITQ 60

Db 1 MKPAREARLPSPRSGRLMALPLLLLLRLGQIILCAGTSPSPIDPSAVATATGSENGITQ 60
QY 61 ISSTASHKONGCTPOVENFNTSEDESSGANDSLRTPGSGNGTGDAGSKTPSTGPS 120
Db 61 ISSTASHKONGCTPOVENFNTSEDESSGANDSLRTPGSGNGTGDAGSKTPSTGPS 120
QY 121 PVFDKAVSIPNTVILTWKNDTRASEYKVVVGHKMEKNTITVHQPCNITGLPAT 180
Db 121 PVFDKAVSIPNTVILTWKNDTRASEYKVVVGHKMEKNTITVHQPCNITGLPAT 180
QY 181 SVFSGITGIGNETWGDPRVILKITEPIPVSDLRVALTGVRKALSMWNGGTASCRVLL 240
Db 181 SVFSGITGIGNETWGDPRVILKITEPIPVSDLRVALTGVRKALSMWNGGTASCRVLL 240
QY 241 ESIGSHEELTQDSLRQVNIIDLKPGVOYNINPYLLQSNKTKGDLPLQKVMMPAIQREAG 300
Db 241 ESIGSHEELTQDSLRQVNIIDLKPGVOYNINPYLLQSNKTKGDLPLQKVMMPAIQREAG 300
QY 301 AGSPFAPVHDSLVGPVDPSSGQSRDTEVLVLGLEPGRYRNATVYSGAANGTEGCPQAI 360
Db 301 AGSPFAPVHDSLVGPVDPSSGQSRDTEVLVLGLEPGRYRNATVYSGAANGTEGCPQAI 360
QY 361 EFRTNALQVFDVAVNISATSLTLIMKVSNDNESSNTYKIHVAGETDSNLNVSEPRAY 420
Db 361 EFRTNALQVFDVAVNISATSLTLIMKVSNDNESSNTYKIHVAGETDSNLNVSEPRAY 420
QY 421 IPRGSRSTFNITICPVLDIEGRGFLQVHTPPVSDRVYVSTTEGLAMSSDAE 480
Db 421 IPRGSRSTFNITICPVLDIEGRGFLQVHTPPVSDRVYVSTTEGLAMSSDAE 480
QY 481 SPQNHITQEGAGNSRVEITTNOSIIIGLPGTKYCEIYKPKGPNTEGASRTVCNRTVP 540
Db 481 SPQNHITQEGAGNSRVEITTNOSIIIGLPGTKYCEIYKPKGPNTEGASRTVCNRTVP 540
QY 541 SAVDIDHVVYVTTTMMMLDMKSPDGASEYHHVLIESKHGSHNTSTYDKAITTQGLPGT 600
Db 541 SAVDIDHVVYVTTTMMMLDMKSPDGASEYHHVLIESKHGSHNTSTYDKAITTQGLPGT 600
QY 601 LYNITISPEVDHWGDNSTAOYTRPSNVSNIDVSTNTTAATLSMWNFDPASPTYSYCLL 660
Db 601 LYNITISPEVDHWGDNSTAOYTRPSNVSNIDVSTNTTAATLSMWNFDPASPTYSYCLL 660
QY 661 IEKAGNSNATQVVTDTGITDAITVTELIIPGSSYTVELFAQVGDGIXLSBGRKSFCTDPA 720
Db 661 IEKAGNSNATQVVTDTGITDAITVTELIIPGSSYTVELFAQVGDGIXLSBGRKSFCTDPA 720
QY 721 SMASFDCEVVPKBPALVLTCTCPPGANAGRELEVSSGAMNNAHTLSCSENGTEYRTYEV 780
Db 721 SMASFDCEVVPKBPALVLTCTCPPGANAGRELEVSSGAMNNAHTLSCSENGTEYRTYEV 780
QY 781 TYLNFSTSYNISITVSCGMAAPTRNTCTTGITDPPPGDSNITSVSHNSKYVFSGF 840
Db 781 TYLNFSTSYNISITVSCGMAAPTRNTCTTGITDPPPGDSNITSVSHNSKYVFSGF 840
QY 841 EASHGPIKAYAVILTTGEAGHPSADVLKTYDDFKKASDPTVYTLIRTEKRGSGSLSE 900
Db 841 EASHGPIKAYAVILTTGEAGHPSADVLKTYDDFKKASDPTVYTLIRTEKRGSGSLSE 900
QY 901 VLKYEIDVGNESITLGYNGKLEPLGSYRACVAFNITFHPONKLTIGASYSYFSFY 960
Db 901 VLKYEIDVGNESITLGYNGKLEPLGSYRACVAFNITFHPONKLTIGASYSYFSFY 960
QY 961 SDAVSLPQDPGVLGAVFGCIFGALVIVVGGFIIPKRRKDAKKNNEVFSQIKPKGSKL 1020
Db 961 SDAVSLPQDPGVLGAVFGCIFGALVIVVGGFIIPKRRKDAKKNNEVFSQIKPKGSKL 1020
QY 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPRYAAELAEENKRNYYNVL.PYDIS 1080
Db 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPRYAAELAEENKRNYYNVL.PYDIS 1080
QY 1081 RVLASVQTHSTDDYINANWMPGHSKKDPFATQGP.LPNTL.KDFWVMEKKNYVAILMLTK 1140
Db 1081 RVLASVQTHSTDDYINANWMPGHSKKDPFATQGP.LPNTL.KDFWVMEKKNYVAILMLTK 1140


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Db      1081 RVLKSVQTHSDTDYINANNYMPGYSKQDFIATQGPLPTLLKDFWRMWEKKNVAIIMLTk 1140
Qy      1141 CVEGGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDPFTYKNIQTSSHPLROPH 1200
Db      1141 CVEGGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDPFTYKNIQTSSHPLROPH 1200
Qy      1201 TSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFIAIDRLIYQIE 1260
Db      1201 TSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFIAIDRLIYQIE 1260
Qy      1261 NENTVDYVGIYDILRMHRPLMNVQTEDOYVFLNQCVLDIRSQKSKVDLIYQNTTAMTY 1320
Db      1261 NENTVDYVGIYDILRMHRPLMNVQTEDOYVFLNQCVLDIRSQKSKVDLIYQNTTAMTY 1320
Qy      1321 ENLAPVTTFGKTNGYIA 1337
Db      1321 ENLAPVTTFGKTNGYIA 1337

RESULT 5
US-10-366-547-47
; Sequence 47, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366.547
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-366-547-47

Query Match      64.1%; Score 4508.5; DB 15; Length 1238;
Best Local Similarity 67.2%; Pred. No. 2.1e-268;
Matches 901; Conservative 108; Mismatches 226; Indels 105; Gaps 12;

Qy      1 MKPAAREKRLPPRSPGLRMALPLILLRLQGLICAGTSPSPIDPPSVATVATGENGITQ 60
Db      1 MKPAAREKRLPPRSPGLRMALPLILLRLQGLICAGTSPSPIDPPSVATVATGENGITQ 60
Qy      61 ISSTAESFHQNGTGPQVETNTSEDSGSGANDSLRTPBOGSGTGDASQKTPSSTGPS 120
Db      61 ISSTAESFHQNGTGPQVETNTSEDSGSGANDSLRTPBOGSGTGDASQKTPSSTGPS 120
Qy      44 ----- 43
Db      44 ----- 43
Qy      121 PVFDIKAVISPTVNIILTKSNDTAASEYKVVYKHMEKNTITVHQPMCNITGLRPAT 180
Db      121 PVFDIKAVISPTVNIILTKSNDTAASEYKVVYKHMEKNTITVHQPMCNITGLRPAT 180
Qy      44 --FIEAV-VSPTSVILTKKINDSGASECR--IEKMESNLTFPKYQNTSCNITGLSPGT 98
Db      44 --FIEAV-VSPTSVILTKKINDSGASECR--IEKMESNLTFPKYQNTSCNITGLSPGT 98
Qy      181 SYVSITGIGNETWGTGDRVIVKVTPEPIPVSDLRALTKVKAALSMNGNGTASCRLL 240
Db      181 SYVSITGIGNETWGTGDRVIVKVTPEPIPVSDLRALTKVKAALSMNGNGTASCRLL 240
Qy      99 SYTFSIISVTNETLNK-----TITTEPWPVSDLHTVSGVTOARLTWNNAGTASLYRLI 154
Db      99 SYTFSIISVTNETLNK-----TITTEPWPVSDLHTVSGVTOARLTWNNAGTASLYRLI 154
Qy      241 ESIGSHHEELQDSRLQVNVISDLKPGVQVNIINPYLL--QSNKTKGDPDLGTEGGGLDASNTERS 299
Db      241 ESIGSHHEELQDSRLQVNVISDLKPGVQVNIINPYLL--QSNKTKGDPDLGTEGGGLDASNTERS 299
Qy      155 EELTTHS-----SVNISGLKPGTN--NTFAPPESENETQADPAVAEEVPDANGTKRI 203
Db      155 EELTTHS-----SVNISGLKPGTN--NTFAPPESENETQADPAVAEEVPDANGTKRI 203
Qy      300 RAGSPFAVHDESLVGPVDPSSGQGSRTDEVLLVGLBEGTRYNATVYSQAANGTEGQPOA 359
Db      300 RAGSPFAVHDESLVGPVDPSSGQGSRTDEVLLVGLBEGTRYNATVYSQAANGTEGQPOA 359
Qy      204 PV-TVLSQLHKNSLYS--VDPSPGQDPSLTETLLTDLKEDTQYNATVYSQAANGTEGQPRN 261
Db      204 PV-TVLSQLHKNSLYS--VDPSPGQDPSLTETLLTDLKEDTQYNATVYSQAANGTEGQPRN 261
Qy      360 IEFPRNAIQVDYVAVNISATSLTITKVSNDNESSANTYKIHVAGETDSSNLVSEPERA 419
Db      360 IEFPRNAIQVDYVAVNISATSLTITKVSNDNESSANTYKIHVAGETDSSNLVSEPERA 419
Qy      262 KVFKNSTQVSDVRAVNISASSMTLTWKSNDGSHTSIVYKIHVAGGTHSVNQTNNKTEA 321
Db      262 KVFKNSTQVSDVRAVNISASSMTLTWKSNDGSHTSIVYKIHVAGGTHSVNQTNNKTEA 321
Qy      420 VIPGLRSTFNITVTCVPLGIDEGTGRPLQVHTPVPVSDFRVTVVSTTEIGLAWSSHDA 479
Db      420 VIPGLRSTFNITVTCVPLGIDEGTGRPLQVHTPVPVSDFRVTVVSTTEIGLAWSSHDA 479

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Db      322 IILGLSSSTLYNITVHFFLQTEGTEGFLQVYSSPDQVSDFRVTVVSTRAIIGLWRNSDS 381
Qy      480 ESPQMHITQGGAGNSRVEITNOSIITGLFPGTKYCFEELVPGPNTEGASRTVCARTV 539
Db      382 KSFEIFIKQDGGEGRRNASIGNOSYWEDELPKGTSHFEELIPKPDGTGELSTVNGSTD 441
Qy      540 PSAVFDIHVVYVTTTMMMLDMKSPDGAEEYVHLVIESKHS--NHTSTYKALITLQGLIP 598
Db      442 PSAVTDIRVNIISTTEQLQENQNTDASGYTHLVLESKSGSIIRNTSSQKMITVGSILP 501
Qy      599 GTLYNITISPEVDHWMDPNSTAQYTRPSNVSNIDVSTNTTAATLSQNFDDASPTYSYC 658
Db      502 GTLYNVTIPEVDQIQGISNSITQYTRPSSVSHLEVNTTTTAAIRKKNDAASASYAYS 561
Qy      659 LLIKAQSSNAQVVT-DIGITDATTETLIPGSSVYVEIFAQVGDGIKSLBPKRSFCT 717
Db      562 VLIKTGDSNVTSNFTKDPSSI--LIPELIPEGSVYTKILTVGGDSTSLVPGMNLFC 618
Qy      718 DPAMASFDCEVVPKEPALVLKMTCPGANAGFELVSGAMNATLHSCSSENGTEYR 777
Db      619 EPEEVTSPKCEVVPKEPALVLKMACPFGMTTGFELGYRSDSMQNMNTLENCTSDDDTECR 678
Qy      778 TEVYINFTSYNISITTVSCGKMAAPTRNTCTGITDPPDPDGSFNITSVSHSVKVF 837
Db      679 TEVAYLNFTSYNISITTVSCGKMALPAQNICTGITDPTPDGSFNITSVSHSVKVF 738
Qy      838 SGFASHGPIKAVAVIITTEGAGHPSADVLTYYTDDPKKASDYYVYLLRTTEKGRSOS 897
Db      739 SGFASHGPIKAVAVIITTEBAAPASADVLTYYTDEKRAASDYYVYLLRIEEKGSGQG 798
Qy      898 LSEVLKYEIDVNGESTTIGYNGKLPELGSYRACVAFNTITFHPQNGKLDGASVYSF 957
Db      799 LSEVLNTEIDVNGOSTLIGYNGRLPELGSYRACVAFNTITVLLQNDGLINGESVYSF 858
Qy      958 SRYSDAVSLPQDPGVICGAVFGCIFGALVITVYVGGFI FWRKRRDAQNEVSFSQIKPKK 1017
Db      859 SPYSEAVFLPQDPGVICGAVFGCIFGALAITAVGFI FWRKRRDAQNEVSFSQIKPKK 918
Qy      1018 SKLIRVENFEAYFPKQADNSCGFAEEYEDKLGVISQPKYAAALANRGNRRNNVLPY 1077
Db      919 SKLIRVENFEAYFPKQADNSCGFAEEYEDKLGVISLKYTAIAANRGNRRNNVLPY 978
Qy      1078 DISRVKLSVQTHSDTDYINANNYMPGYSKQDFIATQGPLPTLLKDFWRMWEKKNVAIIM 1137
Db      979 DISRVKLSVQTHSDTDYINANNYMPGYSKQDFIATQGPLPTLLKDFWRMWEKKNVAIIM 1038
Qy      1138 LTRKCEQGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDPFTYKNIQTSSHPLRQ 1197
Db      1039 LTRKCEQGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDPFTYKNIQTSSHPLRQ 1098
Qy      1198 FHTFSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFIAIDRLIY 1257
Db      1099 FHTFSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFIAIDRLIY 1158
Qy      1258 QIENENTVDYVGIYDILRMHRPLMNVQTEDOYVFLNQCVLDIRSQKSKVDLIYQNTTAM 1317
Db      1159 QIENENTVDYVGIYDILRMHRPLMNVQTEDOYVFLNQCVLDIRSQKSKVDLIYQNTTAM 1218
Qy      1318 TIYENLAPVTTFGKTNGYIA 1337
Db      1219 TIYENLAPVTTFGKTNGYIA 1337

RESULT 6
US-10-366-547-49
; Sequence 49, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE

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; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366,547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1216
; TYPE: PR
; ORGANISM: Rattus norvegicus
US-10-366-547-49

Query Match      64.0%; Score 4499.5; DB 15; Length 1216;
Best Local Similarity 67.1%; Pred. No. 7.3e-268;
Matches 900; Conservative 106; Mismatches 205; Indels 131; Gaps 10;

QY 1 MKPARARLPPSPGRLMLPLLLRLGOLCGGTPSPRPDSVATVATGNGITQ 60
DB 1 MKPARARTRTPSPGRLMLPLLLRLGQGVVCTG----- 37

QY 61 ISSTAESFKONGTGPQVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSGPS 120
DB 38 -----AAS 41

QY 121 PVFDKAVSISPTNVLITWKSNDTASERYVVKHENEKITTVHQPCNITGLRPT 180
DB 42 PVFDVEAVT-SPTSVALTWKNDASATSEYK-----NEGNTLRVTYVNGQTSFNITGLSPAT 96

QY 181 SYVESITPGINETWGDPRVITKITEPIPVSDLRVALTGVRAKALSMKNGNTASGRVLL 240
DB 97 SYFSTITLGVNNTSCKRPYKNTITTEPWPVSDQVAVIGVQALLAMSNANGASTAYRQOI 156

QY 241 ESTGSHELTQDSRLQVNISDLKPGVQVNIINPYLLQSNKTKDPLGTEGGLDASNTERSR 300
DB 157 -----VELTWS--SGGISDLKPGTHKSL--AVQGSNETQHDLMWTE----- 194

QY 301 ACSPTAPVDESLVGPVDPSSGQGSRDTEVLLVGLRGRNATYVSSQANGTEGQPOAI 360
DB 195 -----GVSDPPSADPSLTVEILLTELKPDQYVVTYISQAADTEGQPOAK 240

QY 361 ERTNAIQVDTAVANISATSLTLWKVSDNESSNNTYKIHVAGETOSNLNVEPRAY 420
DB 241 VEKTPDIQVSDIRAVNISDSNMTLWKSNNESHAFYKIIYAGSGSINETVETQAV 300

QY 421 IGLSSTFYNTTCVGLDIEGTGFLQVHTPPVPVSDFRVTVSTTEIGLAMSDDAE 480
DB 301 IGLSSSTLYNTITVPLGQTAGIPGLQVTSPPVSDFRVTVSLREIGLAMSDSE 360

QY 481 SFQMHITQAGANSRVEITTNOSIITIGLFPGTKYCFEIVPGRPGVTEGASRTVCNRTVP 540
DB 361 SPEIFITQGSSEKRNNASTGDLSTYVNLKPGTSYQFEIIFRPGPVGTEGSPQTVVAGKDC 420

QY 541 SAVFDIHVVYVTTTMMWLDKSPDGASEVYHLVLESKHSNHTSTYDKATITLQGLPGT 600
DB 421 SAVTDIRVVSSTTEIQLQEMQNTDASGYTHLVLESNGSIKINSSQKMTTIGGLPGT 480

QY 601 LYNITISPEVHMGDPNSTAQYTRPSNVSNIDVSTNTAATLSMQNDDASPTYSICLL 660
DB 481 LYNVITIFBEVDOMENSSITQYTRPSNVSYIEVNTNTVGAIDWKILDAASASYSYVL 540

QY 661 IEKAGNSSNATQVYTDIGITDATTETELIPGSSYWEIF-----AQVGDGKISLPGKRSF 715
DB 541 ILKADGDSNVTSRVD--IPSVTIPGLIPGVSEYKIFTKIRNTEVGENE---PGQKLF 594

QY 716 CTDPASMASPDCEVVPKRPALVLTWTCPPGANAGBEIEVSSGANNATHTLESSENGTE 775
DB 595 CMEPQVDSLCEVVPKRPALVLTWACPPGNNSGBEIEGVSDADNMNTHLENCTLDNTE 654

QY 776 YRTEVTYANFSTYSYISITTVSCGMAAPRTNCTGTGTDPPPDGSPNTTSVSHNVKV 835
DB 655 CRTEVTYANFSTYSYISATISCGKMLPTOSTCTGTGTDPPPDGSPNTTSVSHNVKV 714

QY 836 KFSGEASHGPIKAVAVILLTGEAGHPADVLKTYTDDFKKGSADTYVTVLIIRTEGGRS 895

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DB 715 KFSGEASHGPIKAVAVILLTGEAGHPSTDLKTYTEDFPKKGSADTYVTVLIIRTEGGRS 774
QY 896 QSLSEVLKXEIDVGNESITLGYNGKLEPLGSYACVAGFTNITFEHPONKGLIDGASVY 955
DB 775 QGLSEALNVEIDVGNOSTLIGYNGRLEPLGSYACVAGFTNITYINQNDGLINGDSYV 834
QY 956 SFSRSDAVSLPQDPGVTCGAVFGCIGFALVITVGGIFEMRRKKRDKAKNNEVSFSQIKP 1015
DB 835 SFSRSDAVSLPQDPGVTCGAVFGCIGFALVIVAGGFIEMRRKKRDKAKNNEVSFSQIKP 894
QY 1016 KKSILIRYENFEAFKKQAOANSCGFAEYEDLKVGSQKYAAELAEKGRKRVNVL 1075
DB 895 KKSILIRYENFEAFKKQAOANSCGFAEYEDLKVGSQKYAAELAEKGRKRVNVL 954
QY 1076 PYDISRVKLSVQTHSTDDYINANYPGYHSKKDFIATQGPLNTLKQFWMVEKKNYAI 1135
DB 955 PYDISRVKLSVQTHSTDDYINANYPGYHSKKDFIATQGPLNTLKQFWMVEKKNYAI 1014
QY 1136 IMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVPEMTIRDPFTYKNIQTSSEHPL 1195
DB 1015 VMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVPEMTIRDPFTYKNIQTSSEHPL 1074
QY 1196 RQFHTSPDHGVDPDTDLLINFRYLVADYMKOSPSPSPILVHCSAGVGTGFIADRL 1255
DB 1075 RQFHTSPDHGVDPDTDLLINFRYLVADYMKOIPSPSPILVHCSAGVGTGFIADRL 1134
QY 1256 IYQIENNTYDVYGVIVDLMHRPLMQTEHDYVFLNQCVLDIVRSQKSVLDIYQNTT 1315
DB 1135 IYQIENNTYDVYGVIVDLMHRPLMQTEHDYVFLNQCVLDIIRAQKSKVDLIYQNTT 1194
QY 1316 AMTIYENIAPVTPFGKNGYIA 1337
DB 1195 AMTIYENIAPVTPFGKNGYIA 1216

RESULT 7
US-10-723-606-3
; Sequence 3, Application US/10723606
; Publication No. US20040161821A1
; GENERAL INFORMATION:
; APPLICANT: Palca-Hamblin, Helena L.
; TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS
; FILE REFERENCE: 200125.447
; CURRENT APPLICATION NUMBER: US/10/723,606
; CURRENT FILING DATE: 2003-11-26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-723-606-3

Query Match      25.8%; Score 1811; DB 16; Length 341;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 RKKRKDAKNNVVSFSQIKPKSKLIRVENFEAFYFKQOADSNGFAEYEDLKVGISQP 1056
DB 1 RKKRKDAKNNVVSFSQIKPKSKLIRVENFEAFYFKQOADSNGFAEYEDLKVGISQP 60
QY 1057 KYAAELAEKGRKRVNVL PYDISRVKLSVQTHSTDDYINANYPGYHSKKDFIATQGPL 1116
DB 61 KYAAELAEKGRKRVNVL PYDISRVKLSVQTHSTDDYINANYPGYHSKKDFIATQGPL 120
QY 1117 PNTLKQFWMVEKKNYAILMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVPE 1176
DB 121 PNTLKQFWMVEKKNYAILMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVPE 180

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QY      123 FDIKAVSISPNVLLTWMSNDTJASSEYKVXKHKEENKTITVHQPCNJTGLPATSU 182
Db      759 FDHEVITIKANKONPLQTYSIP-----KSENE-----CVFQVLPGALY 796
QY      183 VFSITTPGIG---NETWGDPRVIKYITEPIPVSDLRVALTGVRKAALSWSNGNGTASCUV 238
Db      797 SVUTYTTSQGYEANEQ--GNGRTI-----PEPYKDILTNRSTBEDLHWMSGANG----- 844
QY      239 LLSBSIGSHE--ELTODSRFL-----QVNISDLKPQVOY----NINPYLIQSUKT 280
Db      845 ---DVDQYEIQLTFMDMKVPPPFHLVNTATERFTSLTRPGROYKILVLTISGDVQOOSAFI 901
QY      261 KG-----DPLG-----TEGGIDASN-----TESRAGSPAPAHDSL 313
Db      902 EGFIVPSAVKNIHISPNGATDSLTVNMTPGGDDVDVSIVSAFRHSOKDQSOTIPGH---- 957
QY      314 VGVPDPSSGOOSRDTEVLVLGLEPSTRYNATVYSQAANGTEGQPDAIEFTTALJOVEDVT 373
Db      958 -----VEHHTFHRLLEGEQYOIMLAS--VGSILKNQJNVGRITPVASVGQVI 1002
QY      374 AVN-ISA TSLTLINKVSDNESSNYTKIIHVAGETDSSNLVSEBRA-----VIPGL 424
Db      1003 ADNAYSSSYSLIVSQAKAGVAE--RYDILLTENGILLRMTSBPATYKOHKFEDLTLPKG 1058
QY      425 RSSRFMYNTVCPIVLDIGETPGFLQVHPRPVPVPSDFRTLVVVSTTEIGLAWSHDESPQM 484
Db      1060 K-----YKIQILTVSGGLPSKEAQTEGRVPAVIDLRLTENSTRHLSFRWTASBEGELSWY 1115
QY      485 HI---TORGAGNSRUEI--TTNOSIIIGGLFGPTKYCFEIVPKGPNGTEGASTRVNCRITVP 540
Db      1116 NIFLNPBGNIQERAOVDPLVQSFQYLLQGBMVKMWIVTH--SGELSNESFIKGRITVP 1173
QY      541 SAVPDIHVVVYTTTE-MWLDMKSYPDGASEYYVHLVIESKHGSNHTSTYDKAIT--LOGL 596
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RESULT 9
US-09-909-567B-54
; Sequence 54, Application US/09909567B
; Publication No. US20030022257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Selvu
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: dex-0214
; CURRENT APPLICATION NUMBER: US/09/909,567B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21

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NUMBER OF SEQ ID NOS: 56
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 54
 LENGTH: 1997
 TYPE: PRF
 ORGANISM: Homo sapien
 US-09-909-567B-54

Query Match 17.7%; Score 1241; DB 10; Length 1997;
 Best Local Similarity 29.6%; Pred. No. 5.1e-67;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

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QY 123 FDIKAVISPTNVLITWKSNDTAASEYKVVVGHKMEKNTITVHQPMCNITGLRPATSY 182
DB 759 FDHYEVTIKNNKNIQTKSIP-----KSENE-----CVFQVLPGRLY 796
QY 183 VRSITPGIG----NEWGDPRIYKITEPIPSDLRVALTVGRKALMSNGNGTASCRV 238
DB 797 SVTVTTKSGQYEANRG-GNGRTI-----PEPVKDLTLNRSTEDLHVWTSANG----- 844
QY 239 LLESIGSHE--ELTODSRL-----QVNIISDLKPGVOY-----NINPYLLQSNKT 280
DB 845 ---DVDQYEIQLLFNDMKVFPPFHLVNTATREYRFTSLTGRQYKILVLTISGDVQOSAFI 901
QY 281 KG-----DPLG-----TEGLDASN-----TERSRAQSPTAPVHDESL 313
DB 902 EGFTPVSAVKNIHISFNGATDSLTVWMTFGGDDVDSYTVSAFRHSQKVDSCITIPKH----- 957
QY 314 VGPVDPSSGQSRDTEVLLVGLPEGRVNAATVYSGAANGTEGQPAIEFRNALQVFDVT 373
DB 958 -----VEHTHRLHASEQYOIMIAS--VSGSLKNOQINNVGRVTPASVQGYI 1002
QY 374 AVN-ISAATSLTLMKVSDNESSNTYKIHVAGETDSSNLNVEBRA-----VIPGL 424
DB 1003 ANNAVSSYSLIYMWQKAGAVAE--RYDILLITENGILLIRNTESEATTKQKHEDLTPGK 1059
QY 425 RSTSTYNTVCPVLDIESTPGLQVHPVPVSVSPRYTVVSTTEIGLAMSHDASESQM 484
DB 1060 K---YKIQILTSQGLFSKKAQTKGRVPAVATLRLITENSTRILSPFRMASEBELSMY 1115
QY 485 HI---TOGAGNSRVEI--TTNQSIIIGGLPGTKYCFEIVPGKPGTEGASRTVCNRTVP 540
DB 1116 NIFLVNPGNIOERAOVDPVIVGFSFOULLQCRMTKMTIVH--SGELSNESFTRGRTVP 1173
QY 541 SAVFDIHVVYVTTT--MWLDWKSPPDGAEEVYHVLIESKHSNHTSTYDKAIT--LOGL 596
DB 1174 ASVSHLRGSNRTTDSLWFNWSPASGDPDF-YELLVNPNGTKEMKDKDLTEMRFGGL 1232
QY 597 IPGLTYNTISPEVDHVGDPNSTAQYTR-----PSNVSNIDVSTNTAATL-----SMQN 647
DB 1233 VPGKTYLVW---VTHSGDLSNKTATBSRTJAPSPELSMSFADIANTSLATITWKGPPWTD 1289
QY 648 FDDASPTV---SYCLLIEKAGNSNATOVTDIGITDATTVELLPGSSSYTEIPIAQVODG 704
DB 1290 YNDFELQVLPDALTVFNPNYNNRKSERLIYV-----LRPGNSYQNVNATVSGDS 1339
QY 705 IKSL-EPKRSFCTDPASMASFDCVVPKEPALVILKTCPCPGANAGFELEVSSGAMNAT 763
DB 1340 WKTYSKPPIFGSVRRKPKDKIQMLHCR-PONSTAIACSWIPPOSDDGYISIE-----CR 1390
QY 764 HLESQSSNGTEYRETVYLNFE-----STSYNISITTVCGKMAAPRNTCTTGITDPP 818
DB 1391 KMDQOEVEFSKRLKEKESLIMMLVPHKRYLVSIKVOSAGMTSEVEDSTTIDRPP 1450
QY 819 PDGSPNI-----TSVSHSVK--VKSGFEASHGPIKAVAILTTG-----EAGHP 862
DB 1451 P--PPHIVNEKOVLISKSSINFVNCMSWFSDTNGAVKYFTVVVREADGSDDELKPPQHP 1508
QY 863 SADVLKTYDDPKFGASDTTYTYLIRTEBEKRSQSLBSVLKYEIDVANESETTG----- 916
DB 1509 LPSTLYEYHNASIIVYQTNV--FASKCAENPNSNKS-----FNIKLGAEMESIGGKCDPT 1562
QY 917 ---YNGKLEPLGSRACVAGFTNITFHPQNKGLIDGASEVYSR--YSDA-VSLP--- 967

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DB 1563 QOKFQDGLKPHHTVYRISIRAFTO-----LPD--EDIKETPKLYSDTFPSLPITT 1611
QY 968 -QDPGVIGAVFGCIPGALVI---VTVGFIWFRK--RKDAKNNEVSFSQIKP----- 1015
DB 1612 ESEP--LEGAIEGVASAGFLIGMLVAVALLICQKVSHGERSARSALIRDRPLSVHL 1669
QY 1016 -----KSKKLIRVENFEYFFKQOADSNGCAEYEDLKVGISQPKYAAELANRG 1067
DB 1670 NLGQKGNKRTISCPKINQFEGHEFKLOADSNVYLLSKEEYELKQVGRQOSCDIALLPENRG 1729
QY 1068 KNRVNVNLPYDISRHKLS-VQTHSTDDYINANVWPGHSHKDDFATQGPLNTLKDPFRM 1126
DB 1730 KNRVNVNLPYATATVKSNDVDDPCSDYINASYIRGNFRREYIVYQGPLPGTKDPPK 1789
QY 1127 VMEKQVTAIIMLKICEVQGTKEEYPSKO-AQVYGDITVAMTSEIVLBEWTRDPTVK 1185
DB 1790 VMEQNVHNIWVTCQVEKGVKCDHWYPADQDSIYEDLILQMLSESVLPEMTIRREKIC 1849
QY 1186 NIQTSSEHPL-ROPHFTSWPDHGVDPDTDLINFRVYRVMQSPRESFIVHCSAGVG 1244
DB 1850 GEEQDLNRLIRHFTVWPDHGVPEYTGSLQFRTVRYINRSPAGFTVHCSAGVG 1909
QY 1245 RTGTFIADRLIYOIENENTVDVYGVYDLMRMRPLAVQTEQDQVFLNQCVLDIVBSQKD 1304
DB 1910 RTGTFIADRLIQQLDKSDSDVYIGAVHDLRLHVMVQTECQYVYLHQCVRDVLABARKL 1969
QY 1305 SKVDLIYQNTTANTTYENLAP 1325
DB 1970 RS-----EQENPLPEIYENVNP 1986

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RESULT 10

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US-10-408-765A-2135
Sequence 2135, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Boia D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Wainock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088 465
CURRENT APPLICATION NUMBER: US/10/408, 765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2135
LENGTH: 1997
TYPE: PRF
ORGANISM: Homo sapiens
US-10-408-765A-2135

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Query Match 17.7%; Score 1241; DB 16; Length 1997;
 Best Local Similarity 29.6%; Pred. No. 5.1e-67;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

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QY 123 FDIKAVISPTNVLITWKSNDTAASEYKVVVGHKMEKNTITVHQPMCNITGLRPATSY 182
DB 759 FDHYEVTIKNNKNIQTKSIP-----KSENE-----CVFQVLPGRLY 796
QY 183 VRSITPGIG----NEWGDPRIYKITEPIPSDLRVALTVGRKALMSNGNGTASCRV 238
DB 797 SVTVTTKSGQYEANRG-GNGRTI-----PEPVKDLTLNRSTEDLHVWTSANG----- 844
QY 239 LLESIGSHE--ELTODSRL-----QVNIISDLKPGVOY-----NINPYLLQSNKT 280
DB 845 ---DVDQYEIQLLFNDMKVFPPFHLVNTATREYRFTSLTGRQYKILVLTISGDVQOSAFI 901

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QY 281 KG-----DPLG-----TEGLDASN-----TERSRAGSPTAVHDESL 313
Db 902 EGFIVPAVKNIHISPNGATDSLTVNTPGGGDVDSYVSAFRHSQKDSQTIPIKH----- 957
QY 314 VGPVDPSSGQGSRDTEVLVLGLBPGTRYNATVYSGANGTEGQPOALEFRFNAIQVDPVT 373
Db 958 -----VFETHFRLEAGEOYQIMIAS--VSGSLKQINNVGRITVPASVQCVI 1002
QY 374 AVN-ISAATSLTLIKVSDNESSNNTYKIHVAGETSSNLNVSEBRA-----VIPGL 424
Db 1003 ADNAVSSYSLIVSMQKAGVAE--RYDILLTENGILLRNTSEPAATTKQKHFEDLTPGK 1059
QY 425 RSTFTYNTVCPVLDEIGTEGFLQVHTPPVPVDSDFRTVVTSTTEIGLAWSHDAESFQM 484
Db 1060 K-----YKIQILTVSGGLFSKKAQTEGRVPAAVDLRTENSTRLSRMTASBGLSWY 1115
QY 485 HI---TOEGAGNSRVEI-TTNQSIIGGLFPGTKYCFEIVKPGNGTEGASRTVCNRTVP 540
Db 1116 NIFLYNPQNLQEBRAQVDPVLQVSFQNLQGRMYKQVIYTH--SGELSNESFIFGRITVP 1173
QY 541 SAVPDIHVYVYTTTE-WMLDKKSPDGASEVYVYHLVIESKHSNHTSTYDKAIT---LOGL 596
Db 1174 ASVSHLRGNSNNTTDSLMFNMSPASGDPDF-YELLVNPNGTKKENMKDKDLTEMRFGJL 1232
QY 597 IPGTLVNTTISPEVDHVGDNSTAQYTR-----PSNVSNIDVSTNTTAATL---SWQN 647
Db 1233 VPGKRYVLMV---VTHSGDSLKNKYTAESRTAPSPSPSLMSPDIANTSIAITMKGPBMTD 1269
QY 648 PDDASPTY---SYCLLEKAGNSSNATQVTDIGITDATTVELIPGSSYVEIFAQVGDG 704
Db 1290 YNDELELQWLPADALTVPFVYNNRKSEGRIVYG-----LBRGSRGYQNVAKTVSGDS 1339
QY 705 IKSL-EPBRKGFCDPDPMASMFDECEVVKPEPALVLTATCPGGAAGFLLEVSSGAMNAT 763
Db 1340 WKYTSKPLFGSVKRPDKIQNLHCR-PONSTALACSWIPPSDEGYSIE-----CR 1390
QY 764 HLBSCSSENGTEYETEVLYNF-----STSYNISTTYSCGKMAAPTNTCTGTITDPP 818
Db 1391 KMDQOEVFESRKLKESKSLNIMLVPHKRYLVSIKVQSAQMTBSVAVDSITIMIDRPP 1450
QY 819 PDGSPNT-----TSVSHSVK--VKFSGFASHGPIKAVVILTTG-----EAGHP 862
Db 1451 P--PPHIRVNEKDVLISSKSIINFVNCMSFSDTNGAVKCYFVVVREADSDDELKREQOHP 1508
QY 863 SADVLATYDDPKKGAADTYTYLIRTEKGRSOSLSVLAKCIDVGNBSTLIG----- 916
Db 1509 LPSTLEYLRHNASIRYQTNV--FASKCAENPNNSKS---FNIKLAGEMSLGKCDPT 1562
QY 917 ---YNGKLEPLGSYRACVAGFTNTTFHPONKGLIDGASVYSPSR--YSDA-VSLP--- 967
Db 1563 QQKCDGFLKPHYTRISIRAFTO-----LFD--EDLKEFTKPLYSIDTPFSLPITTT 1611
QY 968 -QDBGVICGAVFGCIFGALVI---VTYGGFIEMRK--RKDAKNEVSFSQIKP----- 1015
Db 1612 ESEB--LEGALEGVSAGLFLIGLVAVALLICQKQVSHGREBPSARLISIRDRPLSVHL 1669
QY 1016 -----KSKLIRVENFEAFYKKQADSNCGFAEEEDLKVGISQPKYAAELAEKRG 1067
Db 1670 NLGQGNKRNKTSPIKINQFEHFMKLQADSNVYLSKEYEELKDVGRNOSCDIALLPENRG 1729
QY 1068 KNRNVNVLVYDISRYKLS-YQTHSTDYINANVMPGVSKDQFATQGPLPNTLKDFPRM 1126
Db 1730 KNRNNILPYATKVLKSNVDDDDPCSDYINASYIPGNFRREYIVTQGPLPGETDKDFPKM 1789
QY 1127 VMEKNVVAIIMLTQVCEGRTKCEBWPBSQ-ADYGDITVAMTSEIVLPMTIRDFTVK 1185
Db 1790 VMEQNVHIVMWTQCEVEKGVKCDHYVPADQDSLYGDLILQWSESVLPMTIRREFKIC 1849
QY 1186 NIQTSSEHPL-RQHFHTSWPHGVBDTDLINRIVLYVDYTMKQSPSPSPILVHCSAVG 1244
Db 1850 GEEDLDARILRHPRHYTVMPDHGVETQSLIQFRATRYDIRNSPGAGPTVHCSAVG 1909
QY 1245 RTGFIAIDRLIYQIENENTVDVYGIYVDLHMRHPLMVQTEQVYFLNQCVLIVRSQKD 1304
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Db 1910 RTGFIAIDRLIQGLDSKSDSDYIGAVHDLHFRHVMVQTECOYVYHLQCVRDVLRARL 1969
QY 1305 SKVDLIYQNTAMTIYENLAP 1325
Db 1970 RS---EQENPLFPIYENVNP 1986

RESULT 11
US-10-497-692-4
; Sequence 4, Application US/10497692
; Publication No. US2005004056A1
; GENERAL INFORMATION:
; APPLICANT: Weise, Martin
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Fritsch, Rudiger
; APPLICANT: Hader, Thomas
; APPLICANT: Broemer, Gunter
; APPLICANT: Steuernagel, Arnd
; TITLE OF INVENTION: PP10D, Tec protein tyrosine kinase and EDPp homologous proteins
; TITLE OF INVENTION: involved in the regulation of energy homeostasis
; FILE REFERENCE: 2923-632
; CURRENT APPLICATION NUMBER: US/10/497,692
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/EP02/13744
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: EP 01 000 010.5
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EP 01 129 138.2
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: EP 01 128 844.6
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-692-4

Query Match 17.7%; Score 1241; DB 16; Length 1997;
Best Local Similarity 29.6%; Pred. No. 5.1e-67;
Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

QY 123 FDIKAVSISPTNVLITKSNNTASVYKVKHGMENKITTIVHQPWCNTITGLRPAISY 182
Db 759 FDHYEVITIKKNKNDPIQTKSIP-----KSENE-----CVFQVLVGRLY 796
QY 183 VFSITPGIG---NETGDDPRVIVKITEPIPVSDLRVALTGVKALSMNSGNGTASCRV 238
Db 797 SVYTTTSGQYEANBO-GNGRTI-----PEPVKDLTLRKNSTEDLHTWGSANG----- 844
QY 239 LLESIGSHE-ELTQDSRL-----QVNISDLKPGVQY-----NINPYLLQSNKT 280
Db 845 ---DVDQYEIQLFNMDKVPFPFHLVNTATGYRFTSLTPGQYKILVLTISGVOQSFAFI 901
QY 281 KG-----DPLG-----TEGLDASN-----TERSRAGSPTAVHDESL 313
Db 902 EGFIVPAVKNIHISPNGATDSLTVNTPGGGDVDSYVSAFRHSQKDSQTIPIKH----- 957
QY 314 VGPVDPSSGQGSRDTEVLVLGLBPGTRYNATVYSGANGTEGQPOALEFRFNAIQVDPVT 373
Db 958 -----VFETHFRLEAGEOYQIMIAS--VSGSLKQINNVGRITVPASVQCVI 1002
QY 374 AVN-ISAATSLTLIKVSDNESSNNTYKIHVAGETSSNLNVSEBRA-----VIPGL 424
Db 1003 ADNAVSSYSLIVSMQKAGVAE--RYDILLTENGILLRNTSEPAATTKQKHFEDLTPGK 1059
QY 425 RSTFTYNTVCPVLDEIGTEGFLQVHTPPVPVDSDFRTVVTSTTEIGLAWSHDAESFQM 484
Db 1060 K-----YKIQILTVSGGLFSKKAQTEGRVPAAVDLRTENSTRLSRMTASBGLSWY 1115
QY 485 HI---TOEGAGNSRVEI-TTNQSIIGGLFPGTKYCFEIVKPGNGTEGASRTVCNRTVP 540
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Db      1116 NIFLYNDGNLQSRQAQDPLVQSFQNLQGRMYKAVIYTH--SGELSNESIIRGRTP 1173
Qy      541 SAYVDIHVVYVTTT-MWLDKSPDASSEVYHVLVIESKGSNHTSTYDKAIT--LOGI 596
Db      1174 ASVSHLGSNRNNTTDSLMFNWSPASGDPDF-YELILYNPGTKKEMWKDKDLEMFQGL 1232
Qy      597 IPGTLVNTISPEVDHWGDPNSTAGYTR-----PSNVSNIDVSTNTAATL-----SMON 647
Db      1233 VPKRKVLMV---VTHSGDLNKNVTAESRTAPSPSLMSFADIAINTSLAITWKGPDPWTD 1289
Qy      648 FDDASPTY---SYCLLEKAGNSNATQVVTDTGTDATVTELLIPSSYVLEIFAQVGDG 704
Db      1290 YNDFELQWLPDALTGFNPNYNNRKSGRIVYG-----LRGRSQGVNWKVYSGS 1339
Qy      705 IKSL-EPGRKSFCTDPAASMASPDCEVVPKEPALVTKTGPANAGFELEVSAGMANNAT 763
Db      1340 WKYTSKPIGSAVTKKDKIQNLHCR-PONSTALACSWIPDSDPDFGYSIE-----CR 1390
Qy      764 HLESCSENGTEYRTVYTLNF-----STSYNISITTVSCGKMAAPTRATCTGTDP 818
Db      1391 KMDTOEVEFSRKLKESKSLNIMLVPHKRYLVSIVQAGMTSEVEDSTITMIDRPP 1450
Qy      819 PDGSPNI-----TSVSHSVK--VKSGFEASHGPIKAVAVILTTG-----EAGHP 862
Db      1451 P--PPHIRVNEKDVILASKSINFETVNCWFSPTNGAVKFTVVEADGSDDELKPEQGH 1508
Qy      863 SADVLKTYVDDFKGASDYYVYTLIRTEKGRSQSLSEVLKXIDVGNSTTLG----- 916
Db      1509 LPSYLELRNASTRIYQYNY--FASKCANPNNSNS--FNILKGMESLGSKDPT 1562
Qy      917 ---YNGKLEPLGSAVCAVAFNTITFHQKGLIDGASVYSFSR--YSDA-VSLP--- 967
Db      1563 QOKFCGPIKPHYATYISIRAFQ-----LFD--EDLKEFTKPLYSDFSLPTT 1611
Qy      968 -ODPGVIGAVFGCIFGALVI---VTYGGFIEMRK--RKDAKNNVYSFSQIKP----- 1015
Db      1612 ESEF--LFGALIGVSAHGLFLIGMLVAVALLCRKGVSHGRPARLSIRDRPLSVHL 1669
Qy      1016 -----KSKLIRVENFEAFYFKQADNSCGFAEEYEDLVISOPKTAABLAENRG 1067
Db      1670 NLGQKGNRTSCPIKINQEGHFMLOQADSNVLSKEYELKDVGRNOSCIALLPENRG 1729
Qy      1068 KRRYNNVLPYDISRYKLS-VQTHSTDDYINANPFGYHSKDFIATQGPLFNILKDFWRM 1126
Db      1730 KRRYNNILPYDATRYKLSNVDDPCSDYINASYIRGNFRREYIVTQGPLFGTKDDFWKM 1789
Qy      1127 VKEKNVYALIMLTKEGORTKCEEYWPSCO-AQDYGDITVAMTSEIYLPMTIRDPYVK 1185
Db      1790 VWEQVNHNIWVYTCVEKGRVCKDIYMPADODSLYTGDLIQMLSESVLPMTIRREFKIC 1849
Qy      1186 NIQISESHPL-RQHFHTSMPDHGVDPDTDLLINFRYLRVDMYKOSPPEPSPLVHCSAGV 1244
Db      1850 GEEQLDAHRLIRHFHYTWPDPHGVPEITQSLIQFRTRYDYLINSPGAGPFIYVHCSAGV 1909
Qy      1245 RTGTIALIDRLIYOENENTDVYIVDILMRHPLMQTDEQYVFNLOCYLDIVRSOKD 1304
Db      1910 RIGFIADRLIQOQDSKOSVDIYGAVHDLRLHVRVQTECOYVYVHOCVRAVLRARL 1969
Qy      1305 SKVDLIYONTTAMTIYENIAP 1325
Db      1970 RS---EQENPLFIYENVNP 1986

RESULT 12
US-10-497-692-14
; Sequence 14, Application US/10497692
; Publication No. US20050004056A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Fritsch, Rüdiger
; APPLICANT: Hader, Thomas

; APPLICANT: Bromner, Gunter
; APPLICANT: Steuereagel, Arnd
; TITLE OF INVENTION: PPI10D, Tec protein tyrosine kinase and EDRP homologous proteins
; TITLE OF INVENTION: Involved in the regulation of energy homeostasis
; FILE REFERENCE: 2923-632
; CURRENT APPLICATION NUMBER: US/10/497,692
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/EP02/13744
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: EP 01 000 010.5
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EP 01 129 138.2
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: EP 01 128 844.6
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-692-14

Query Match      17.5%; Score 1230; DB 16; Length 1450;
Best Local Similarity 29.3%; Pred. No. 1.5e-66;
Matches 390; Conservative 197; Mismatches 495; Indels 250; Gaps 53;

Qy      125 IKAVISPT---NVILTKSNDTPAASEYRYVVKH-----KMEKKTITVHQP 169
Db      216 VQGVSVNSARSIDLRIYSWHAATGDPDHYEVTKIKNNNFQTSKIPSENE----- 266
Qy      170 WCNTIGRPATSVYFSTIPGIG---NETWGDRVIVKITEPIPVSDIKALTVKAKAL 225
Db      267 -CVVQVLVPGRLYSVTYTGSGYEABEQ-GNCRIT---PEPVADLTLRNSTEDLVH 319
Qy      226 SWSNGNGTASCRLLESIGSHE--ELTODSRL-----QVNIISDKPGVOY----- 268
Db      320 TWSCANG-----DVDQYEIQLLFNDKVPFPHLVNVAIEYFSTLTPRQVKILV 370
Qy      269 -NINPYLQSNKTKG-----DPIG-----TEGGLDASN-----TERSR 300
Db      371 LTISGVDQSAFIEGFTVPASVAKNIHISPQATDSLTVNWTGGGVDVDSYVSAFHSOK 430
Qy      301 AGSPFAVHDESLVGPVDPSSGQOSRDTEVLVGLPGRYNAVTVYSGANGREGQPAI 360
Db      431 VDSQTIPIKH-----VFHTPHRLAAGQIQIMTAS--VSGSLKQIIV 471
Qy      361 EPRTNALQVFDVAVN-ISAATSLILMKVSDNESSNTYTKIHVAGETDSNINLNVSEPPA 419
Db      472 VGRTPASVQGVYADNAVSYSLSIVSMQKAGVAB--RYDILLLTENGILRLNRTSEPAT 528
Qy      420 -----VIRGRASFTFNITVCPVLGPIEGPGLQVHTPRVPVSDPRVNVSTIEIG 471
Db      529 TKQHKKEDELTPGKK---YKIQTLTVSGGLFSKKAQTEGRVPAATVTLRITENSTRHLS 584
Qy      472 LAWSHSDASFOVHI---TOEGAGNSRVEI--TTNOSIIIGGLFPGTKYCFEIVPGRPNT 527
Db      585 FRNTASBEGELSWNIIPLVNDGNLQRAQVUDLVQSFQNLQGRMYKAVIYTH--SGE 642
Qy      528 EGASRTVCNRTVPASAVFDIHVVYVTTT-MWLDKSPDASSEVYHVLVIESKGSNHTST 586
Db      643 LSNESFIFGRTPASVSHLRGSNRNNTTDSLMFNWSPASGDPDF-YELILYNPGTKKENW 701
Qy      587 YDKAIT---LOGIIPGTLVNTISPEVDHWGDPNSTAGYTR-----PSNVSNIDVSTNT 638
Db      702 KQKDLTEMFQGLVGRKIVLMV---VTHSGLSKNVTAESRTAPSPSLMSFADIAINTS 758
Qy      639 TAATL---SWONFDDASPTY---SYCLLEKAGNSNATQVVTDTGTDATVTELLIPGS 691
Db      759 LAITWKGPDPWTDYNDFELQWLPDALTGFNPNYNNRKSGRIVYG-----LRGR 808
Qy      692 SYTVLEIFAQVGDIGSL-EPGRKSFCTDPAASMASPDCEVVPKEPALVTKTGPANAGF 750

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Db 809 SYQENKTVSGDWMKTSKPIFGSVTRPKDIONLHCR-PONSTAIACSWIPDSDPDGY 867
Qy 751 ELEYSAGMANNATHLESSENGTEYREYVLYNF-----STSVNISTTVSCGMAMPT 805
Db 868 SIE-----CRKNDIOBEVFSRKLKESKSLNMLVPHKRYIVSTIKVOSAGTSEBV 919
Qy 806 RNTCTTGITDPPPGSGPNI-----TSVSHSVK--VKFSGFEASHPIKAYAVILTTG 857
Db 920 EDSTITTMIDRRPP--PHIRVNEKDVLISKSSINFNTNCSWFSPTNNAVKFYVVAEA 977
Qy 858 -----EAGHPASADVLKTYTDFPKKASDPTVYTYLLIRTEBKRSQSLSEVLKYEIDVG 909
Db 978 DGSDELKEQOHPLEPSYLEYRHNASIRVYQNTY--FASKCAENPNSNKS-----FNILKG 1031
Qy 910 NESTTLG-----YNGKLEPLGSYRACVAGTNTTTPHONKGLIDGAEYSYFSR- 959
Db 1032 AEMESLGGKCDPTQOKFCDDGLKPTAYRISRATQ-----LFD--EDLKEPTKP 1080
Qy 960 -YSDA-VSLP-----ODPGVICGAVFGCIFGALVI---VTVGGFIFMRKK---RKDAKNE 1007
Db 1081 LYSDFEFLPITTESEP--LFGALIGVAGLEFLIGMLVAVALLICRQVHGHRERSAR 1138
Qy 1008 VSPFOIKP-----KSKLIVENFEAVFKKQADNSCGFAEYEDLXLVGIS 1054
Db 1139 LSIHRDRPLSVHNLGQKGNKRTSCPIKINQFEGHFMLQADSNYLSKEYEELKDVGRN 1198
Qy 1055 QPKAAELAEHRGKRYNNULPYDISRYKLS-VQHSITDDYINANMYGHSKDFIATQ 1113
Db 1199 QSCDIALPERGKRYNNILPYDATRYKLSNVDDPCSDYINASYIIGNNFRERYIATQ 1258
Qy 1114 GPLFNTLKDFFRMWEKUNVAILMLTKCEQRTCESEYFWSKQ-AQDYGITVAMTSEI 1172
Db 1259 GPLGCTKDDFKMWEQONVHNIWMTQCEVKRGVCHYWRPADQSLYGGDLILQMSSES 1318
Qy 1173 VLPEWTRDFTVKNIQTSSEHPL-RQHFTSMPDHGVDTTDLINFRYLVADYKQSP 1231
Db 1319 VLPEWTRDFTVKNIQTSSEHPL-RQHFTSMPDHGVDTTDLINFRYLVADYKQSP 1378
Qy 1232 ESPLVHNSAGVGRGTIAIDRLIYQENENTVUVGIVDRLMRHLMQTEQYVFL 1291
Db 1379 AGPVTWHCSAGVGRGTIALDRLIYQENENTVUVGIVDRLMRHLMQTEQYVFL 1438
Qy 1292 NQCVLDIVRSOK 1303
Db 1439 HQCVRDVLRARK 1450

RESULT 13
US-10-245-539-2
: Sequence 2, Application US/10245539
: Publication No. US20030077638A1
: GENERAL INFORMATION:
: APPLICANT: Logan, Thomas Joseph
: TITLE OF INVENTION: MID 4460, A HUMAN TYROSINE PHOSPHATASE
: FILE REFERENCE: MP101-155P1RM
: CURRENT APPLICATION NUMBER: US/10/245,539
: PRIOR FILING DATE: 2002-12-05
: PRIOR APPLICATION NUMBER: 60/323,018
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 1118
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-245-539-2

Query Match 16.1%; Score 1130; DB 14; Length 1118;
Best Local Similarity 25.9%; Pred. No. 1,5e-60;
Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

Qy 8 ARLPRSPG-----LRWALPLLLLLRLGQILCAGGTSPSPIDPSPVATVAT 53

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Db 25 ARAPAPNGRNLIVETQTTSSISLSMEVP-----DGLDS--QNSVWVOCT 68
Qy 54 GENGITQISAEFPHQNGTGTPOVETNSEDSESGA--NDSLRTPQGSNGTDAQ 111
Db 69 GGGGTTERTNT-----TATNTVDDLGRPSLYTGSVWEKQDVSNSVGT- 112
Qy 112 KTPSTGSPVPDIKAVISPTVILITKMSNDTASEYK-VYVGHKNEK--TITVHQ 168
Db 113 -VTTATAPNVRNLRVBAQTNSIALITWEVVDGDPQNSITGYVYTGDDGAGRSTAH- 170
Qy 169 PWCNIT--GLRPATSYFSTIPGIGNETWGDPRVIKVIITEPIPVSLRLVALTGVKALS 226
Db 171 --TNTVDELPGCLVAFSM----- 188
Qy 227 WSNNGRASCVRLESIGSHELTQ---DSRLQVINIDLKPGVQYNNIPYLQSNKTKG 282
Db 189 WVGKNGINSSRETNNATTAHPNVRKPPSGSDHQLHLPEL--GGRMH--RPPELLRLTSA 246
Qy 283 DPLGTEGLDASNTERSRAGSPTPAVHDESLVGPVDPSSGQSRDETVILVLEPGTFRN 342
Db 247 LEMVAEQRLTQPTES-----PVD-----GLGRGSLYT 275
Qy 343 ATVYSQANGTEGQPOAIEFTNAIOVEDVTAVANISATSLTLIKVSDNESSNYTKIH 402
Db 276 CSWVEKQGVNSSMBRLVTSITTAHPNVRNLTVEAQNTSSIALITWEVDPDPQNSYGYE 335
Qy 403 VAGETDSNINLVSPPRAVITPGLASSTFNITVCVGLDIBETPGLQVH----- 451
Db 336 YTGQGRA-----GTRSTAHNTIVDL--EPCLLYFVSVWGNKINS 377
Qy 452 -----TPVPVSDFRVTVVSTTEIGLAWSSDAE-----SFOMHTOGAGNRYEI 498
Db 378 SRETRNATTAPNVRNLMETQNTSSIALCHEVDGEPPOLYTYWGTGCG--GGETERN 436
Qy 499 TTNOSIIIGLFPQTKYCFELIVPKNTEGASRTVCNRYPSAVFDIHVVYVTTKML 558
Db 437 TTNSTVTAERLEPGLTFTFSVMAE-KNGARGSNVNSISTVPAVNTSLSKQDMNTSLAL 495
Qy 559 DWKSPD--GASEYYHL--VIESKGSNHSITDKAIIITQGLIGTLNITISEVDHW 614
Db 496 RMTAPQPGQSSYSYVWVSWVEGMTDPRQSTGDTITLKLKELGSLHLLVMAERNEVR 555
Qy 615 GDPNSTAQYRPSVNSINDVSTNTTAATLSQNF--DDASPTYGYCLIEKAGN----- 666
Db 556 GYNSTLTRAIPANEVITDQNETQTKNSVLMWKAPGDPHSQLYVWVQWASKGPRQGD 615
Qy 667 -SSNATQVYVTDIGITDAVTELEIPGSSYVEIFAQVGDGIKSLBGRKSPC--TDPASMA 723
Db 616 PQAMVWQTSRNTNTWYKVEALEPGLTYNFTVMAERNDVASSTQ---SLCASTYPTVT 671
Qy 724 SPDCVVPKEPALVUKTQCPGANGAFLEVYSSGAMNATHLESSENGTEYREYVYL 783
Db 672 ITSCVSTISAGVNLIMSCPGGYEAPELEV-----GGCRGSDRS----- 712
Qy 784 NFSTSYNISITTVSCGMAAFTNTCTGIDPPPPGSPNITSVSHSVKXSGFEAS 843
Db 713 -----SCGEAVS-----VLGL----- 723
Qy 844 HGPIKAVAVILITTEAGHPASADVLKTYTDFPKKASDPTVYTYLLIRTEBKRSQSLSEVLK 903
Db 724 -GPASVYATITT-----IWDGK-----VVS 744
Qy 904 YEIDVGNESITLGYNGKLEPLGSYRACVAGTNTTTPHONKGLIDGAEYSVFSRSDA 963
Db 745 HSVVCHTESA----- 754
Qy 964 VSLPQDGVICGAVFGCIFGALVITVVGFIEMRKGRDAKNEVSPQIKPKSKL--- 1020
Db 755 -----GVLAGAVVGLI--LFLIVGLILFPLKRRKKK-----QKPELRDLVFS 797
Qy 1021 -----IRVENFEAVFKKQADNSCGFAEYEDLXLVGISQPYAAELAEHRGKRYNNVLP 1076

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Db      798 SPGDIPADFPADHVRKNERDSNCGFADEYQOLSLVHGSQOMVASASENNAKRYRNVLP 857
Qy      1077 YDISRYKLS-VQTHSTDDYINANMPGYHSHKQPIAIOGRLPNTLADFPAMWEKXVYAI 1135
Db      858 YDMSRVPLKPIHEPBGSDYINASFMPGLMSPQEFIAIOGRLPQTVGDFPRLVWEQOQSHTL 917
Qy      1136 IMLTKEVQGRTKCEEYWP-SKQADYGDITVAMTSEIYLPENTIRDFYKNIQTSSEHP 1194
Db      918 VMLTNCMEAGRVCCEHYWPLDSQPCCTGHRLRVTLVGEWEWMENTVARELLLOVEBQKTL 977
Qy      1195 LROFHFTSWPDHGVDPDTLLINFRYLVRDYMKOSPESPILVHCSAGVGRGTFTAIIR 1254
Db      978 VRQFHVQAMPDHGVPSPTLLAFWRMLRQMDQYMEGGPPIVHCSAGVGRGTFTIADLV 1037
Qy      1255 LIYOIENENTVDYVGIYVYDLRMHRPLMVQTEDOYVFLNOCVLDIVRSQ 1302
Db      1038 LMLQLOSEGLGPFSPFRKMRRESRPLMVQTEAOYVFLHQCIGSSNSQ 1085

RESULT 14
US-10-245-539-8
; Sequence 8, Application US/10245539
; Publication No. US20030077638A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: MID 4460, A HUMAN TYROSINE PHOSPHATASE
; FILE REFERENCE: MP101-155PIRM
; CURRENT APPLICATION NUMBER: US/10/245,539
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 60/323,018
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 1118
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-245-539-8

Query Match      16.1%; Score 1130; DB 14; Length 1118;
Best Local Similarity 25.9%; Pred. No. 1.5e-60;
Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

Qy      8 AALLPSPSPG-----LKWALFLILLIRLGOILCAGGTPSPIDPSPVATVAT 53
Db      25 AAAPAPNPGRLVTETQTSSISLSWEVP-----DGLDS--QNSNYVQCT 68
Qy      54 GENGITQISSTASFFHKQNGTGPQVETNTSDEGSSGA--NDSLRTGQSGNGTDASQ 111
Db      69 GGGGTTERTNT-----TATNVYDGLGPGSLYTCSVWEKDGVSNGSVGT-- 112
Qy      112 KTPSSTGSPVPFDIAVSIPTNVLLTWKSNDDTASEYK-YVVKHKKMENEK--TITVVHQ 168
Db      113 -VTITATNPVNTLHVEAQINSSIALTWEVDPGPDPQNSTGYVEITGCGGAAGRSTAH- 170
Qy      169 PWCNTT-GIARATSVYSITPGIGNEFWGDPRIYKVTTEPIPVSDLRVALTVRKAL 226
Db      171 --TNTVLDGLEPGCLYAFSM-----PVD-----GGPGSLYLT 275
Qy      227 WSNNGTASCVLLESIGSHELTQ---DSRLQVNIIDLKRGVQYINIPYLLQSNKTKG 282
Db      189 WVGKNGINSRETRNATTAHNPVRKRPESGSDHQLHLP-L-GGRRW-HRTELDLNTISA 246
Qy      283 DPLGTGGLDASNTERSPASPAPVHDESLVGPVDPSSGOQSRDTEVLVGLPRTRYN 342
Db      247 LEMVAERLELTQOTPEP-----PVD-----GGPGSLYLT 275
Qy      343 ATVYSAANGTEGQPOAIEFRITNAIQYEDYAVNAISATSLTLWKVSDNESSNYTYKIH 402
Db      276 CSVWEKGVGNSSSRWLVTSTTANPNRNLVTEAQINSSIALTWEVDPGPDPQNSTGYVE 335
Qy      403 VAGETDSSNLNVSEPRAVIPGLRSTFYNIIVCPVLADIGTGPGLVH----- 451

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Db      336 YTGDSGRA-----GTRSTAHNTITVDRL-----EPGLYVFSVWVGKNGINS 377
Qy      452 -----TPVPVSDFRVTVVSTTEIGLAWSSHDAE-----SPQMHITQAGANSRREI 498
Db      378 SRETNATTAHNPVNTLHVEAQINSSIALTWEVDPGPDPQNSTGYVEITGCGGAAGRSTAH- 436
Qy      499 TTNQSIITIGLFPFGTKYCFELVPRKQPNTEGASRTVCNRTPVAPVDIHVVYVTTTMM 558
Db      437 TYNSTVTAERLEPGLTYFYSVWAE-KNGARGSRQNVSIIVPNAVTSLSKQDWTNSTIAL 495
Qy      559 DKSPPD--GASEYVYHL--VIESKHGSHNTSYKATITLQGLIGTLYNTITISEVHW 614
Db      436 RMTAPQGGQSSYSTVWSVWREKMTDPTOSTGSTDTITLKELEGLSYHLITVMAERNEVR 555
Qy      615 GDNSTAOYTPRSVNSINDVSTNTTAATLSWQNF--DASPTYSYCLLIEKAGN----- 666
Db      556 GYNSTLTAAATAPNEVTDLQNETQTKNSVMLMWKARQDPHSQLYVYVWQWASKHPRRGD 615
Qy      667 -SSNATQVYVDIGITDATTVELIGSSYVYEIFAQVDDGIKSLERPKSPC--TDPASMA 723
Db      616 PQAMVWNTSKTNETWYKVEALEBGLTNFTVMAERNDVASSTQ---SLCASTYPPDTVT 671
Qy      724 SPDCEVVPKEBALVIAKWTCPPGANAGFELEYSNGAMNATHLSCSENGTERTVETYL 783
Db      672 ITSCVSTISAGVNLINSCQGGYEALELEY-----GGQRQSQRS----- 712
Qy      784 NFSTSVNISITVWSCGKMAAPTRNTCTTGITDPPPDGSENIITSVNSVYKVPFGREAS 843
Db      713 -----SCGAVS-----VLGL----- 723
Qy      844 HPIKAYAVILTTGEAHPADVLKTYDDPFKGAASDTYTYLIRTEBKRSQSLSEVYLK 903
Db      724 -GPARSIPATITTT-----IWDGK-----VVS 744
Qy      904 YEIDVGNESFTLLGYNKLKPLGSRVACVAGFTNTTFHPQNKGLIDGAEYSVFSRYSDA 963
Db      745 HSYVCHTESA----- 754
Qy      964 VSLPQDPGVICGAVFGICFALVIVYVGGFIPIFRKRRKADKANNEVSPQIKPKSKYL--- 1020
Db      755 -----GVLAGAPVGLL--LFLILVGLIFPLKRRNKK-----QOKELRLDLPVS 797
Qy      1021 -----IRVENFEAYFKQOADSNGCFABEYEDLTVLGISOPKYAAELAEKRGKRYNVLP 1076
Db      798 SPGDIPADFPADHVRKNERDSNCGFADEYQOLSLVHGSQOMVASASENNAKRYRNVLP 857
Qy      1077 YDISRYKLS-VQTHSTDDYINANMPGYHSHKQPIAIOGRLPNTLADFPAMWEKXVYAI 1135
Db      858 YDMSRVPLKPIHEPBGSDYINASFMPGLMSPQEFIAIOGRLPQTVGDFPRLVWEQOQSHTL 917
Qy      1136 IMLTKEVQGRTKCEEYWP-SKQADYGDITVAMTSEIYLPENTIRDFYKNIQTSSEHP 1194
Db      918 VMLTNCMEAGRVCCEHYWPLDSQPCCTGHRLRVTLVGEWEWMENTVARELLLOVEBQKTL 977
Qy      1195 LROFHFTSWPDHGVDPDTLLINFRYLVRDYMKOSPESPILVHCSAGVGRGTFTAIIR 1254
Db      978 VRQFHVQAMPDHGVPSPTLLAFWRMLRQMDQYMEGGPPIVHCSAGVGRGTFTIADLV 1037
Qy      1255 LIYOIENENTVDYVGIYVYDLRMHRPLMVQTEDOYVFLNOCVLDIVRSQ 1302
Db      1038 LMLQLOSEGLGPFSPFRKMRRESRPLMVQTEAOYVFLHQCIGSSNSQ 1085

RESULT 15
US-10-245-539-4
; Sequence 4, Application US/10245539
; Publication No. US20030077638A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: MID 4460, A HUMAN TYROSINE PHOSPHATASE
; FILE REFERENCE: MP101-155PIRM

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CURRENT APPLICATION NUMBER: US/10/245,539
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: 60/323,018
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1093
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus sequence
US-10-245-539-4

Query Match      16.0%; Score 1127; DB 14; Length 1093;
Beet Local Similarity 26.3%; Pred. No. 2,2e-60;
Matches 344; Conservative 177; Mismatches 418; Indels 350; Gaps 37;

QY 53 TGENGITOISSTAESHKQNGTGPQVETNTSEDESSGA--NDLRTPEQSGNGTDGAS 110
DB 43 TGDGTTETRT-----TATNTYVDLGGSLYTCGVWWEKGVNSVGT- 87
QY 111 QKTPSTGSPVFDIKAVISPTNVLTKSNDTASEYK-YVVKHKNENEK--TITVH 167
DB 88 --VTATAPNPNRNLRAQNTSSIALTWEVDPDPQNSTGYVEYTGDDGAGTRSTAH 145
QY 168 QPMCHIT--GIRPATSYFSTITPGIGNETWGDPRVIXITEPIVSDLRVALTVRKAL 225
DB 146 ---TNTYDGLPEGLVAFSM----- 163
QY 226 SMSNGTASCRVLLLESIGSHELTQ---DSRLQVNSDLKPGVQYVNIPLQSNKTK 281
DB 164 -WVGKNGNSRETRNATTAAHPVAKPKPSSGSDHQLHPEL-GGPRMH-RPELDLRTS 220
QY 282 GDPLETCGLDASNTERSRAGSPTRPVHDESLVGPVDPSSGQSRDTEVLLVLEPGTRY 341
DB 221 ALEWVAEQRLFTQTPES-----FVD-----GLGPGSLY 249
QY 342 NATYVSOAANGTEGQPAIEPTNAIQVPDYAVANISATSLTKVSDNESSNYTKI 401
DB 250 TCSVWVEDGVNSSSWRLVTSTTAPNPNRLTVEAQNTSSIALTWEVDPDPQNSTYGV 309
QY 402 HVAGETDSNINVSPPRAVIFGLASSTFYNTVCPVLGDIETPGFLQVH----- 451
DB 310 EYTDGDA-----GTRSTANTNITVDRL-----EPGCLYFVSVMGKNGIN 351
QY 452 -----TPPVVSDFRVTVVSTTEIGLAWSSHAD-----SFQMHITQEGAGNSRVE 497
DB 352 SSRERNAATTAPNPNRLHMETQNTSSIALCWEVPDPGYPODYTWVGVTGDDG--GGTEFR 410
QY 498 ITTNOSIIIGLFPETKYCFELVPGKPGNGTEGASRTVCNRTYPSAVFDIHVVYVTTTBMW 557
DB 411 NTYNTSVTAERLEPGLTLYFSVMAE--KNGARSRQNVISITVPNAVTSLSKQDWTNSTIA 469
QY 558 LDMKSPD--GASEVYVYH--VLESKGSNHTSTYDKAITLOGLIPGLYNITISPEVDHV 613
DB 470 LRMTPAQPGGSSSYWVSWVREGMTDPRTOSTSGTDITLKELENGSLHLLTWAEKNEV 529
QY 614 WGDPNSTAQYTRPSNVSNIDVSTNTTAATLSWQNF--DDASPTYSCULLIERKAGN----- 666
DB 530 RGVNSTLTAATAPNNEVTDLOMETQTKNSVLMWKARPDHSQLVYVWQMASKGRPRGQ 589
QY 667 --SSNATOVVTDIGITDATTVELIPGSSYVTEIFAQVGDGKISLEPRGKSPC--TDPASM 722
DB 590 DPOAMVMVQTSKTNETWYKVEALEPGLTYNFTVMAERNDVASSTQ---SLCASTYPDIV 645
QY 723 ASPDEVPKBPALVLYKWTCPGANAGFELEVSSGAMNNAHTLBSCSSENGTEVTEVTV 782
DB 646 TITSCVTSAGCVNLWSCPGGGAPELEV-----GGQKGSQDRS----- 687
QY 783 INFSTSYNISITTVSCGKMAAFTRTCTGTIDPPPPDGSPIITSVSHNSVVKFSGFEA 842
DB 688 -----SCGEAVS-----VLGL----- 698
```

```
QY 843 SHGPIKAYAVLLTTEAGHGPSADVLYKTYDDPFKKGASDTVYTYLLRTEEKRSQSLSEVL 902
DB 699 --GPASTPATIT-----IWMCK-----VV 718
QY 903 KYEIDVGNSTTLLGYNGKLEPLGSRACVAGFTNTTFHPQNKGLIDGASVVSFSRYSD 962
DB 719 SHSVVCHTESA----- 729
QY 963 AVSLPQDPGVICGAVFGCIFBALVIVTVGGLIFPKRKKRKAQKNNVSRQIKPKKSKY-- 1020
DB 730 -----GVYAGAFVGI--LFLILVGLLIFPLKRRKKK-----QOKPELRDLVF 771
QY 1021 -----IRVENFEAFKKQOADSNGCFABEYEDLKLVGISOPKYAAELAEKGRYNNVL 1075
DB 772 SSPGDIPEADPADYKRNKRNSNGCFADETQQLSLVGHSSQGMVYASANNKRRYRNVL 831
QY 1076 PYDISRVKLS-VQTHSTDDYINANYMPQYHSKKQFIATQGLPNTLKDQFWWWEKUNYA 1134
DB 832 PYDMSRVPLKPIHEPQSDYINASFMPGLMSPQEFIAQGPLQTVGDFWRLVWEEQSHT 891
QY 1135 IIMTKCYEGQRTKCEBYWP-SKQADYGDITVAMTSEIYLPWTIRDFYVKNIQTSSEH 1193
DB 892 LVMELTNCMEAGRVCCEHYWPLDSQCTGHRLVTLVGEVEMNTVRELILLQVEEQKTL 951
QY 1194 PLRQFHTSWPDHGVPTDOLLINFRYLVRDYMKSPPESPILVHCSAGVGTGFIAD 1253
DB 952 SVRQFHTQAMPDHGVSSPDTLLFMRMLRQMLQTMGEGFPYHCSAGVGTGTLIAD 1011
QY 1254 RLIVQIENENTVDYGIYVDLRMRPLMVQTEDDQVFLNQCVLDIVSQ 1302
DB 1012 VLNQLQSEGLGPFSPFRKKRSRPLMVQTEADYVFLHQICICSSNSQ 1060
```

Search completed: May 10, 2005, 19:09:31
Job time : 189 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: May 10, 2005, 18:54:46 ; Search time 53 Seconds
(without alignments)
2427.204 Million cell updates/sec

Title: US-09-516-728A-4
Perfect score: 7030
Sequence: 1 MKPARARARLPERRSGLRWA.....TIVENLAPVTTFKTINGYIA 1337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6826	97.1	1337	1	protein-tyrosine-p
2	4508.5	64.1	1238	2	HBP beta-like tyr
3	1242	17.7	1997	1	protein-tyrosine-p
4	1130	16.1	1118	1	protein-tyrosine-p
5	1028	14.6	1630	2	protein-tyrosine-p
6	1026	14.6	1557	2	protein-tyrosine-p
7	981.5	14.0	583	2	protein-tyrosine-p
8	957.5	13.6	1711	1	protein-tyrosine-p
9	954	13.6	1767	2	protein-tyrosine-p
10	949	13.5	1615	2	protein-tyrosine-p
11	879	12.5	1912	2	protein-tyrosine-p
12	864	12.3	2302	2	protein-tyrosine-p
13	854	12.1	1188	1	protein-tyrosine-p
14	842	12.0	1187	1	protein-tyrosine-p
15	839	11.9	1216	2	protein-tyrosine-p
16	834.5	11.9	1621	2	protein-tyrosine-p
17	832	11.8	1691	1	protein-tyrosine-p
18	829	11.8	1894	2	protein-tyrosine-p
19	817	11.6	1367	2	protein-tyrosine-p
20	807	11.5	1898	2	protein-tyrosine-p
21	795.5	11.3	1863	1	protein-tyrosine-p
22	792.5	11.3	1897	1	protein-tyrosine-p
23	787.5	11.2	1907	2	protein-tyrosine-p
24	785.5	11.2	1452	1	protein-tyrosine-p
25	771.5	11.0	1452	1	protein-tyrosine-p
26	767	10.9	1437	2	protein-tyrosine-p
27	764	10.9	1437	2	protein-tyrosine-p
28	761	10.8	2051	2	protein-tyrosine-p
29	750	10.7	2029	1	protein-tyrosine-p

30	742	10.6	1499	2	protein-tyrosine-p
31	739.5	10.5	1501	2	protein-tyrosine-p
32	728.5	10.4	1262	1	protein-tyrosine-p
33	728.5	10.4	1496	1	protein-tyrosine-p
34	722.5	10.3	405	2	protein-tyrosine-p
35	722.5	10.3	405	2	protein-tyrosine-p
36	704	10.0	2314	1	protein-tyrosine-p
37	693	9.9	1585	2	protein-tyrosine-p
38	688.5	9.8	1440	2	protein-tyrosine-p
39	678.5	9.7	1457	1	protein-tyrosine-p
40	674.5	9.6	1301	1	protein-tyrosine-p
41	669	9.5	1445	1	protein-tyrosine-p
42	664	9.4	1442	1	protein-tyrosine-p
43	656.5	9.3	1422	2	protein-tyrosine-p
44	640.5	9.1	1435	2	protein-tyrosine-p
45	636.5	9.1	1304	1	protein-tyrosine-p

ALIGNMENTS

RESULT 1
138670 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human
N:Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase
C:Species: Homo sapiens (man)
C>Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004
C:Accession: 138670; 152599
R:Ostman, A.; Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A:Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced
A:Reference number: 138670; PMID:95024024; PMID:7937872
A:Accession: 138670
A:Molecule type: mRNA
A:Residues: 1-1337 <RES>
A:Cross-references: UNIPROT:Q12913; EMBL:U10886; NID:9558754; PID:9558755
A:Experimental source: HeLa cells
R:Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.
Blood 84, 4186-4194, 1994
A:Title: Molecular cloning, characterization, and chromosomal localization of a novel pr
A:Reference number: 152599; PMID:95086212; PMID:7994032
A:Accession: 152599
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-216, 'LNGVRRKA', 225-260, 'G', 262-285, 'GNEGGLDASNTERRSA', 302, 'S', 304, 'TAPVHDE
A:Cross-references: GB:D37781; NID:9633072; PID:BA07035.1; PID:9633073
C:Comment: Enhanced expression of this protein with increasing cell density suggests a r
C:Genetics:
A:Gene: GDB:PTPRJ
A:Cross-references: GDB:1385040; OMIM:600925
A:Map position: 19q13.4-19q13.4
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
A:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repea
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT>
F:118-197/Domain: fibronectin type III repeat homology <3FNB>
F:206-283/Domain: fibronectin type III repeat homology <3FNB>
F:284-356/Domain: fibronectin type III repeat homology #status atypical <3FNC>
F:365-445/Domain: fibronectin type III repeat homology <3FNB>
F:453-530/Domain: fibronectin type III repeat homology <3FNB>
F:539-617/Domain: fibronectin type III repeat homology <3FNB>
F:720-804/Domain: fibronectin type III repeat homology <3FNB>
F:972-988/Domain: transmembrane #status predicted <TMN>
F:1065-1287/Domain: protein-tyrosine-phosphatase homology <PYP>
F:72, 82, 93, 104, 142, 172, 192, 231, 258, 276, 342, 351, 376, 391, 396, 413, 501, 525, 536, 582, 603, 6
F:1239/active site: Cys (phosphotyrosine intermediate) #status predicted
F:1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 97.1%; Score 6826; DB 1; Length 1337;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1303; Conservative 5; Mismatches 29; Indels 0; Gaps 0;

```

QY      1 MKPAREARLPSPSPGLRMLPLLLLLRLGLLCACTSPSPIDPSVATVAANGENGITQ 60
DB      1 MKPAREARLPSPSPGLRMLPLLLLLRLGLLCACTSPSPIDPSVATVAANGENGITQ 60
QY      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEPOGNGTGDASQKTPSSSTGPS 120
DB      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEPOGNGTGDASQKTPSSSTGPS 120
QY      121 PVVDIAVASISPTNNVLLTWKSNNTASEYKYVVKHMEKEKITTVAHQWCNITGLRPAIT 180
DB      121 PVVDIAVASISPTNNVLLTWKSNNTASEYKYVVKHMEKEKITTVAHQWCNITGLRPAIT 180
QY      181 SYVFSITPGIGNETWGDPRVIKITYTEPIPVSDLRVALTGVRAKALSMNGNGTASGRVLL 240
DB      181 SYVFSITPGIGNETWGDPRVIKITYTEPIPVSDLRVALHAGEBEGCSLSMSNGNGTASGRVLL 240
QY      241 ESIGSHBELTODSRLOVNIIDLKPGVQVINIPYLLQSNKTKGDPLEGEGGLDASNTERSR 300
DB      241 ESIGSHBELTODSRLOVNIIDLKPGVQVINIPYLLQSNKTKGDPLEGEGGLDASNTERSR 300
QY      301 AGSPFAPVHDESLVGPVDPSSGQOSRDTEVLLVGLRPRNATVYSSQANGTGEGQOPAI 360
DB      301 AGSPFAPVHDESLVGPVDPSSGQOSRDTEVLLVGLRPRNATVYSSQANGTGEGQOPAI 360
QY      361 EFRINAIOVEDYAVANISATSLTLTWKSDNESSSNYTKIHVAGETSSNINVESEPAV 420
DB      361 EFRINAIOVEDYAVANISATSLTLTWKSDNESSSNYTKIHVAGETSSNINVESEPAV 420
QY      421 IGLRSTSTYNTTCVGLDIEGTGPFLOVHPVPVSDPRVTVSTTEIGLWAMSHDAE 480
DB      421 IGLRSTSTYNTTCVGLDIEGTGPFLOVHPVPVSDPRVTVSTTEIGLWAMSHDAE 480
QY      481 SFQOMHITOGGANSRVEITTNOSIIIGLFGPKTKCFELVPGMPGTGASRTVCNRTVP 540
DB      481 SFQOMHITOGGANSRVEITTNOSIIIGLFGPKTKCFELVPGMPGTGASRTVCNRTVP 540
QY      541 SAVFDIHVVYVTTTMMWMDWKSPPDGASEYVHLVIESKHSNHTSTYDKAITLQGLIPGT 600
DB      541 SAVFDIHVVYVTTTMMWMDWKSPPDGASEYVHLVIESKHSNHTSTYDKAITLQGLIPGT 600
QY      601 LYNITISPEVDHVMGDPNSTAQYTPSNVNSINDVNTNTAALSMQONDDASPTYSYCLL 660
DB      601 LYNITISPEVDHVMGDPNSTAQYTPSNVNSINDVNTNTAALSMQONDDASPTYSYCLL 660
QY      661 IEKANSSNATQVVTDDIGITDATTVELIPGSSYVTEIFAQVGDGKSLRPERKSFCTDPA 720
DB      661 IEKANSSNATQVVTDDIGITDATTVELIPGSSYVTEIFAQVGDGKSLRPERKSFCTDPA 720
QY      721 SMASTDCVVPKEPALVLTCTPPGANAAGFELFVSSGAMNNATHLSCSSENGTEYRTREV 780
DB      721 SMASTDCVVPKEPALVLTCTPPGANAAGFELFVSSGAMNNATHLSCSSENGTEYRTREV 780
QY      781 TYLANSTSTNISITTVSCGKMAAPTRNTCTGIDTPPPDPSPNTTSVSHSVYKSGF 840
DB      781 TYLANSTSTNISITTVSCGKMAAPTRNTCTGIDTPPPDPSPNTTSVSHSVYKSGF 840
QY      841 EASHGPIKAYAVIILTTGAGHPADVLKTYDDFKKASDITYVYLLRTEBKGHSQSISE 900
DB      841 EASHGPIKAYAVIILTTGAGHPADVLKTYDDFKKASDITYVYLLRTEBKGHSQSISE 900
QY      901 VLKYEIDVGNSTTLGYTNGKLEPIGSRACVAGTNTTTPONKGLDGAESYVSFRY 960
DB      901 VLKYEIDVGNSTTLGYTNGKLEPIGSRACVAGTNTTTPONKGLDGAESYVSFRY 960
QY      961 SDAVSLPODPGVICGAVFGCIFGALVITVGGFIFMRKRDADANNEVSFSQIPKSKL 1020
DB      961 SDAVSLPODPGVICGAVFGCIFGALVITVGGFIFMRKRDADANNEVSFSQIPKSKL 1020
QY      1021 IRVENFEAYFKKQADSNCGFAEEYEDLKLVGISQPKYAAELANRGNRNNTVLPYDIS 1080
DB      1021 IRVENFEAYFKKQADSNCGFAEEYEDLKLVGISQPKYAAELANRGNRNNTVLPYDIS 1080

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QY      1081 RYKLSVQTHSTDDYINANMYGHSKDPFIATQGPLNTLKDQFMRWKEKNVYAIIMLT 1140
DB      1081 RYKLSVQTHSTDDYINANMYGHSKDPFIATQGPLNTLKDQFMRWKEKNVYAIIMLT 1140
QY      1141 CVEQRTCEEYWPBQKQADGIDITVAMTSEIIVPEWMTIRDFYKNIQTSSEHPLRQPHF 1200
DB      1141 CVEQRTCEEYWPBQKQADGIDITVAMTSEIIVPEWMTIRDFYKNIQTSSEHPLRQPHF 1200
QY      1201 TSPDPHGVPTDITLLINFRYVDRYMKQSPESPILVHCSAGVGTGFIADRLIYQIE 1260
DB      1201 TSPDPHGVPTDITLLINFRYVDRYMKQSPESPILVHCSAGVGTGFIADRLIYQIE 1260
QY      1261 NENTVDVGIYYDLMRMRPLWQTEDOYVFLNQCULIVSQRXKVDLYQNTAMTIY 1320
DB      1261 NENTVDVGIYYDLMRMRPLWQTEDOYVFLNQCULIVSQRXKVDLYQNTAMTIY 1320
QY      1321 ENLAPVTTFGKTNGYIA 1337
DB      1321 ENLAPVTTFGKTNGYIA 1337

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RESULT 2

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S68700
HPTP beta-1-like tyrosine phosphatase precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68700
R:Kutamotoch, S.; Matsumoto, S.; Saitoh, T.; Ohnogi, M.; Yamamoto, T.
FBS Lett. 378, 7-14, 1996
A:Title: Molecular cloning and characterization of ByP, a murine receptor-type tyrosine k
A:Reference number: S68700; MUID:96140699; PMID:8549806
A:Accession: S68700
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1238 <ROR>
A:Cross-references: UNIPROT:Q64455; GB:D45212; NID:g1208432; PIDN:BA08146.1; PID:g120843
C:Genetics:
A:Map position: 281-2
C:Superfamily: protein-tyrosine-phosphatase, receptor type U; fibronectin type III repeat
C:Keywords: phosphoprotein
P:1-28/Domain: signal sequence #status predicted <SIG>
P:29-1238/Product: HPTP beta-1-like tyrosine phosphatase #status predicted <MAT>
P:267-347/Domain: fibronectin type III repeat homology <3PR>
P:966-1188/Domain: protein-tyrosine-phosphatase homology <PPP>
F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1146/Binding site: substrate phosphate (Arg) #status predicted

```

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Query Match          64.1%; Score 4508.5; DB 2; Length 1238;
Best Local Similarity 67.2%; Pred. No. 1,5e-244;
Matches 901; Conservative 108; Mismatches 226; Indels 105; Gaps 12;

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QY      1 MKPAREARLPSPSPGLRMLPLLLLLRLGLLCACTSPSPIDPSVATVAANGENGITQ 60
DB      1 MKPAREARLPSPSPGLRMLPLLLLLRLGLLCACTSPSPIDPSVATVAANGENGITQ 60
QY      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEPOGNGTGDASQKTPSSSTGPS 120
DB      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEPOGNGTGDASQKTPSSSTGPS 120
QY      121 PVVDIAVASISPTNNVLLTWKSNNTASEYKYVVKHMEKEKITTVAHQWCNITGLRPAIT 180
DB      121 PVVDIAVASISPTNNVLLTWKSNNTASEYKYVVKHMEKEKITTVAHQWCNITGLRPAIT 180
QY      181 SYVFSITPGIGNETWGDPRVIKITYTEPIPVSDLRVALTGVRAKALSMNGNGTASGRVLL 240
DB      181 SYVFSITPGIGNETWGDPRVIKITYTEPIPVSDLRVALTGVRAKALSMNGNGTASGRVLL 240
QY      241 ESIGSHBELTODSRLOVNIIDLKPGVQVINIPYLLQSNKTKGDPLEGEGGLDASNTERSR 300
DB      241 ESIGSHBELTODSRLOVNIIDLKPGVQVINIPYLLQSNKTKGDPLEGEGGLDASNTERSR 300
QY      301 AGSPFAPVHDESLVGPVDPSSGQOSRDTEVLLVGLRPRNATVYSSQANGTGEGQOPAI 360
DB      301 AGSPFAPVHDESLVGPVDPSSGQOSRDTEVLLVGLRPRNATVYSSQANGTGEGQOPAI 360
QY      361 EFRINAIOVEDYAVANISATSLTLTWKSDNESSSNYTKIHVAGETSSNINVESEPAV 420
DB      361 EFRINAIOVEDYAVANISATSLTLTWKSDNESSSNYTKIHVAGETSSNINVESEPAV 420
QY      421 IGLRSTSTYNTTCVGLDIEGTGPFLOVHPVPVSDPRVTVSTTEIGLWAMSHDAE 480
DB      421 IGLRSTSTYNTTCVGLDIEGTGPFLOVHPVPVSDPRVTVSTTEIGLWAMSHDAE 480
QY      481 SFQOMHITOGGANSRVEITTNOSIIIGLFGPKTKCFELVPGMPGTGASRTVCNRTVP 540
DB      481 SFQOMHITOGGANSRVEITTNOSIIIGLFGPKTKCFELVPGMPGTGASRTVCNRTVP 540
QY      541 SAVFDIHVVYVTTTMMWMDWKSPPDGASEYVHLVIESKHSNHTSTYDKAITLQGLIPGT 600
DB      541 SAVFDIHVVYVTTTMMWMDWKSPPDGASEYVHLVIESKHSNHTSTYDKAITLQGLIPGT 600
QY      601 LYNITISPEVDHVMGDPNSTAQYTPSNVNSINDVNTNTAALSMQONDDASPTYSYCLL 660
DB      601 LYNITISPEVDHVMGDPNSTAQYTPSNVNSINDVNTNTAALSMQONDDASPTYSYCLL 660
QY      661 IEKANSSNATQVVTDDIGITDATTVELIPGSSYVTEIFAQVGDGKSLRPERKSFCTDPA 720
DB      661 IEKANSSNATQVVTDDIGITDATTVELIPGSSYVTEIFAQVGDGKSLRPERKSFCTDPA 720
QY      721 SMASTDCVVPKEPALVLTCTPPGANAAGFELFVSSGAMNNATHLSCSSENGTEYRTREV 780
DB      721 SMASTDCVVPKEPALVLTCTPPGANAAGFELFVSSGAMNNATHLSCSSENGTEYRTREV 780
QY      781 TYLANSTSTNISITTVSCGKMAAPTRNTCTGIDTPPPDPSPNTTSVSHSVYKSGF 840
DB      781 TYLANSTSTNISITTVSCGKMAAPTRNTCTGIDTPPPDPSPNTTSVSHSVYKSGF 840
QY      841 EASHGPIKAYAVIILTTGAGHPADVLKTYDDFKKASDITYVYLLRTEBKGHSQSISE 900
DB      841 EASHGPIKAYAVIILTTGAGHPADVLKTYDDFKKASDITYVYLLRTEBKGHSQSISE 900
QY      901 VLKYEIDVGNSTTLGYTNGKLEPIGSRACVAGTNTTTPONKGLDGAESYVSFRY 960
DB      901 VLKYEIDVGNSTTLGYTNGKLEPIGSRACVAGTNTTTPONKGLDGAESYVSFRY 960
QY      961 SDAVSLPODPGVICGAVFGCIFGALVITVGGFIFMRKRDADANNEVSFSQIPKSKL 1020
DB      961 SDAVSLPODPGVICGAVFGCIFGALVITVGGFIFMRKRDADANNEVSFSQIPKSKL 1020
QY      1021 IRVENFEAYFKKQADSNCGFAEEYEDLKLVGISQPKYAAELANRGNRNNTVLPYDIS 1080
DB      1021 IRVENFEAYFKKQADSNCGFAEEYEDLKLVGISQPKYAAELANRGNRNNTVLPYDIS 1080

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Db 204 PV-TNLSQHLKHSLS-VDPSSGQDPSLTLLTDLKPDQYNATIVSQAANGTEGQPRN 261
Qy IEFRTNALOVDPVATVAVNISATSLTIKVSNDNESSNTYKIHVGEFDSNLVNSEBRA 419
Db 262 KVFKNSTQVSDVNRMINISASSMTLTKNSNDGSTSTSVYKIHVAGTHSVNQVANKKEA 321
Qy 420 VIPGLRSSTFNITVCPVLGDIETGPGFLOVHTPPVPVSDPRVTVSTTEIGLAWSSDA 479
Db 322 IILGSSSTLVNITHPFLGREGFPGFLQVYTSDDQSDPRVTVSTRALGLAMRSDS 381
Qy 480 ESPQMHITQEGAGNSRVEITTNQSIIGLPEPTKYCEIIVPKGNGTEGASRTVCNRTV 539
Db 382 KSFEPIKQDGEKERNASTGQSYVEDLKGTSYHEIILPRGPDGTEGLSTYNGSTD 441
Qy 540 PSAYVDIIVVYVTTTEMLDMKSPGASEVYVHIVIEKHS-NTSTRYDALITQGLIP 598
Db 442 PSAYVDIIVVYVTTTEMLDMKSPGASEVYVHIVIEKHS-NTSTRYDALITQGLIP 501
Qy 599 GTLVNITISPEVDHWGDPNSTAQYTRPSNVSNIDVNTTPTATLSMGNFDDASPTYSYC 658
Db 502 GTLVNITISPEVDHWGDPNSTAQYTRPSNVSNIDVNTTPTATLSMGNFDDASPTYSYC 561
Qy 659 LLIEXAGNSSNAQVYT-DIGITVATVTELLIPGSSYVFEIQAQVGDGKSLBPGKSFCT 717
Db 562 VLILKTDGDSNVTSTFTDPSI-LIPELIPGVSYTKILITQVGDGTTSLVPGWNLFC 618
Qy 718 DPASASDFCEVVPREPALVLTCTPPRANGFELVSSGAMNNAITHESGSENGEYR 777
Db 619 EPEPTSTHCEVVPREPALVLTCTPPRANGFELVSSGAMNNAITHESGSENGEYR 678
Qy 778 TEVTYLNSTSYNISITTVSCGKMAPTNCTTITPPPPDGSPNITSVSHNVKXKF 837
Db 679 TEVTYLNSTSYNISITTVSCGKMAPTNCTTITPPPPDGSPNITSVSHNVKXKF 738
Qy 838 SGFEASHQPIKAYAVILTTGEAHSADVLTCTYDFFKASDIYVYVLIITEKGRSQS 897
Db 739 SGFEASHQPIKAYAVILTTGEAHSADVLTCTYDFFKASDIYVYVLIITEKGRSQS 798
Qy 898 LSEVLKTYIDVNGESTTIGYNGKLEPIGSTRACVAGTNTTFHQNGLIDGASYSYF 957
Db 799 LSEVLKTYIDVNGESTTIGYNGKLEPIGSTRACVAGTNTTFHQNGLIDGASYSYF 858
Qy 958 SRYSDAVSLPODPGICGAVFGCIGALVITVVGFIEMRKRRKQAKNNVFSQIKPKK 1017
Db 859 SRYSDAVSLPODPGICGAVFGCIGALVITVVGFIEMRKRRKQAKNNVFSQIKPKK 918
Qy 1018 SKLIRVENFEAYFKKQADSNCGFAEYEDLKLIGISLPKTYAETAEKRRKRYNNVLPY 1077
Db 919 SKLIRVENFEAYFKKQADSNCGFAEYEDLKLIGISLPKTYAETAEKRRKRYNNVLPY 978
Qy 1078 DISRYKLSVQTHSTDDYINANMPGYHSGKOPFATQGPLPNTLKPFRMVMKKNYALIM 1137
Db 979 DISRYKLSVQTHSTDDYINANMPGYHSGKOPFATQGPLPNTLKPFRMVMKKNYALIM 1038
Qy 1138 LTKCEYQGRTCCEYWPSPKQADYDITVAMTSEIVLPEWTRIDPTVKNIQTSSEHPLRQ 1197
Db 1039 LTKCEYQGRTCCEYWPSPKQADYDITVAMTSEIVLPEWTRIDPTVKNIQTSSEHPLRQ 1098
Qy 1198 FHFTSWPDHGVDTDLLINFRYLVRYDMKQSPESPILLVHCSAGVGTGTFIADRLIY 1257
Db 1099 FHFTSWPDHGVDTDLLINFRYLVRYDMKQSPESPILLVHCSAGVGTGTFIADRLIY 1158
Qy 1258 QIENENTVDYGIYVDLPMHRPLMQTEDOYVFLNQCLDIYRSQKSKDILLYQNTTAM 1317
Db 1159 QIENENTVDYGIYVDLPMHRPLMQTEDOYVFLNQCLDIYRSQKSKDILLYQNTTAM 1218
Qy 1318 TIYENLAPVTTPGKNGYIA 1337
Db 1219 TIYENLAPVTTPGKNGYIA 1238

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RESULT 3
S12050

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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S12050; S15818; S15819
R:Kruiger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A>Title: Structural diversity and evolution of human receptor-like protein tyrosine phos
A:Reference number: S12049; MUID:9106018; PMID:2170109
A:Accession: S12050
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1997 <KRU>
A:Cross-references: UNIPROT:P23467; GB:X54131; NID:935787; PIDN:CAA38066.1; PID:935788
R:de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
FEBS Lett. 282, 285-288, 1991
A>Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.
A:Reference number: S15818; MUID:91243813; PMID:1645282
A:Accession: S15818
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1911, 'VAMVLOK' <VRI>
A:Accession: S15819
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1997 <VR2>
C:Genes:
A:Gene: GDB:PTPRB; PTPB
A:Cross-references: GDB:127352; OMTM:176882
A:Map position: 12q15-12q21
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <W>
F:23-1625/Domain: extracellular #status predicted <EXT>
F:1626-1642/Domain: transmembrane #status predicted <TM>
F:1643-1997/Domain: intracellular #status predicted <INT>
F:1727-1952/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1904/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1910/Binding site: substrate phosphate (Arg) #status predicted

Query Match 17.7%; Score 1242; DB 1; Length 1997;
Best Local Similarity 29.6%; Pred. No. 4.1e-61;
Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

Qy 123 FDIKAVGISPPNVILTKMSNTTASSEYKVVYKMKMENEKTTTVHQPKWCNTGLRPAATSY 182
Db 759 FDHYEVITKKNKNTIQTSLP-----KSEK-----CVFVLVPGRLY 796
Qy 183 VFSITPGIG---NETMGDPVIVIKVTEPIVPSDLRVALTGVRKALSMNGNGTASGRV 238
Db 797 SVYITTKSGQYEANEG-GNGRTI-----PEVVDLTLNRSTEDLHVTMSGANG----- 844
Qy 239 LLESTIGHE--ELTQDSRL-----OVNISDLKPGVQY-----NINPYLIQSNKT 280
Db 845 ---DVDQYEQILLFNDMKVFPFPHLVNTATYRFTSLTPRGQYKILVLTIGDVOQSFAFI 901
Qy 281 KG-----DPLG-----TEGLDLSN-----TSSRAGSPAPRHDSL 313
Db 902 EGFIVPSAVKNIHISPNKATDSLTVNMTPGGGDVDSYTSVAFRRHSQKSDSOTIPGH---- 957
Qy 314 VGPVDPSSGQGSRLTEVLVLGLPEPTRYNATVYVQAANGTEGQPOAIEFRTNALOVDPVT 373
Db 958 -----VFETHFHLLEAGEQVQIMIAS--VSGSLKNGQNVVGRVTPVPSVQSVI 1002
Qy 374 AVN-ISAATSLTLIMKVSNDNESSNVTYKIHVAGETSDSNLVSEBRA-----VIPGL 424
Db 1003 ADNAYSSYLIVSQKAGVAE---RYDILLTLNGLILRNTSEBATTQKHFEDLTPGK 1059
Qy 425 RSTFTYNTVCPVAGDIEGTGFLQVHTPPVPVSDPRVTVSTTEIGLAWSSDAESQW 484
Db 1060 K---YKIQILTVSGGLESKAQTEGRVPAVVDLRTENSTHRLSRMTASBGLSWY 1115
Qy 485 HI---TQEGAGNSRVEI-TTNQSIIGGLPGTKYCEIIVPKGNGTEGASRTVCNRTVP 540

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Db      1116 NIFLYNDGNLQERAGVDPLVQSFSPONLQGRMTVMVLYTH--SELSNESIFERTY 1173
Qy      541 SAFFDHHVYVVTTE-MLDMKSPDQASEVYHVLVESKSGNSHTTYKAT--LQGL 596
Db      1174 ASVSHLRGNSRNTTDSLWFNWPASDPDF-YELIYNPGTKCKENWKCKDKLWEMFOGL 1232
Qy      597 IPGLYNTITISPEVDHVMGDPNSTAQYTR-----PANVSNDVSTNTTATL-----SWGN 647
Db      1233 VPERKTVLWV---VTHSGDLSNKVTHMESKRAPSPPLMFPADIANSLAITKGPDPMD 1289
Qy      648 FDASPTV---SYCLIEKAGNSNAQTQVYTDIGTDAITVBLIPSSYVEIFAQVGDG 704
Db      1290 YNDFELQWLPBDALTFVNPYNNKSEGRITVYG-----LRPGRSYQFVWKTVSGDS 1339
Qy      705 IKSL-EPGRKSFCTDASMASFDCVVPKRPVLVLMKTCPPQANMGELEVSAGMNNAT 763
Db      1340 WKTYSPKPIGSAVTKTKDKIQLHCR-PQNSTALACSWIPDDSDPDGYSIE-----CR 1390
Qy      764 HESCSSENGTEYRETVYLN-----STVNSITVSCGKMAAPTNTCTTGITDPP 818
Db      1391 KMDQVEFESRKLEKESKLINTIMLVPHKRYLVSIKVGAGMTSEVEDSTITMIDRPP 1450
Qy      819 PDGSPVI-----TSVSHSVK--VAFSGFEASHGPTKAYVILTTG-----EAGHP 862
Db      1451 P-PPHIRNEKQVILSKSINFVNCWFSQDNGAVKFTVVEADSGDELKPEQOHP 1508
Qy      863 SADVLKYTDDEPKGASDTYVYLYLIRTEKGRSSQSLSEVLKYEIVQNESTTG----- 916
Db      1509 LSYLEYRNNASIRVQNTY--FASGCAENPNSNGS---FNILGAMESLGKGRDPT 1562
Qy      917 ---YNGKLEPISYRACVAGFTNITFHPQKGLIDGASVYSFSR--YSDA-VSLP--- 967
Db      1563 QOKFCGCPKPHATAVISIRAFQ-----LFD--EDLKEFTKPLYSDTFFSLPTT 1611
Qy      968 -ODPGVIGAVFGCIFGLVLI---VYGGFIWRKK---RKDAKNVYSFSQIKP----- 1015
Db      1612 ESEP--LFGALIGVSAGLFLIGMLVAVALLCRKVSHGRPPARLSIRDRPLSVHL 1669
Qy      1016 -----KSKKLIRENFEAFKTKQADNSCGFAEEYEDLKLVGISOPKYAAELAEENRG 1067
Db      1670 NLGQGNRTSCPIKINGEFGHFMLOQDSNVLISKYEHLKQVGRANSQDIALPEKRG 1729
Qy      1068 KRRYNNVLPYDISRYKLS-VQTHSTDDYINANNYFGHSKQFIATQGPLPNTLKDFWRM 1126
Db      1730 KRRYNNILPYDATRYKLSNVDDDDPCSDYINASYIPGNFRREYITQGPLGTQKDDFWKM 1789
Qy      1127 VKEKNVVAIIMLTCKVEQGRTCCEEYWPCKO-AQYGDITVAMTSEIPLPMTIRDFTVK 1185
Db      1790 VMEQVNHIVWVTCQVEKGRVCKDHWPADDDSLYTGDLILQMLSESVLPMTIRREFKIC 1849
Qy      1186 NIQISESHPL-RQHFSTMPDHGVPDITDLINFRYLRVDYWKOSPSPESPLIVHCSAGV 1244
Db      1850 GEEQDARHLIRHFHYTWPDHGVPEITQSLIQFRTVRDYINSPGAGPVIYVHCSAGV 1909
Qy      1245 RTGTGIALDLILYOENENTDVVGIYVLDLKHRLMQLQEDQYVFLNQCYLDIVRSQKD 1304
Db      1910 RTGTGIALDLILQDSDSDVIGYADVHLRLHVRVMQTECQYVYLHQCVRRVILRAKL 1969
Qy      1305 SKVDLIYQNTTAMTIENLAP 1325
Db      1970 RS-----EQENPLFPIYENVP 1986

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RESULT 4

A49724
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
 N:Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SAP-1
 C:Species: Homo sapiens (man)
 C>Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C/Accession: A49724
 R/Matcozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K.
 J. Biol. Chem. 269, 2075-2081, 1994

A:Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase and
 A:Reference number: A49724; MUID:94124561; PMID:8294459
 A:Accession: A49724
 A:Molecule type: mRNA
 A:Residues: 1-1118 <MATO>
 A:Cross-references: UNIPROT:Q15426; GB:DL5049; NID:g475003; PIDN:BA03645.1; PID:g475004
 C:Gene: GDB: PTRH, SAP-1
 A:Cross-references: GDB:305504
 A:Map position: 19q13.4-19q13.4
 A>Note: highly expressed in colon and pancreatic cancer cells but not in the normal cells
 C:Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repeat
 C:Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric monoest
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:27-110/Domain: fibronectin type III repeat homology <3FNA>
 F:28-1118/Product: protein-tyrosine-phosphatase, receptor type H #status predicted <MAT>
 F:28-761/Domain: extracellular #status predicted <EXT>
 F:116-199/Domain: fibronectin type III repeat homology <3FNB>
 F:205-289/Domain: fibronectin type III repeat homology <3FNC>
 F:296-379/Domain: fibronectin type III repeat homology <3FND>
 F:385-468/Domain: fibronectin type III repeat homology <3FNE>
 F:474-558/Domain: fibronectin type III repeat homology <3FNF>
 F:564-658/Domain: fibronectin type III repeat homology <3FNG>
 F:667-737/Domain: fibronectin type III repeat homology <3FNG>
 F:762-778/Domain: transmembrane #status predicted <TM>
 F:779-1118/Domain: intracellular #status predicted <INT>
 F:846-1070/Domain: protein-tyrosine-phosphatase homology <PP1>
 F:325-78, 83, 107, 132, 149, 172, 196, 203, 286, 304, 312, 329, 352, 376, 383, 401, 436, 439, 470, 490, 558, 5
 F:1022/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1028/Binding site: substrate phosphate (Arg) #status predicted

Query Match 16.1%; Score 1130; DB 1; Length 1118;
 Best Local Similarity 25.9%; Pred. No. 3, 1e-55;
 Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

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Qy      8 ARLPKSPG-----LRMALPLLLLLRLGLCAGTSPSPIDPSVATVAT 53
Db      25 ARAAPAPGRNLIIVETQTSISLSWEV-----DGLDS--QNSNMYVQCT 68
Qy      54 GENQITQISSTABEFHQNQTGTPQVETNSDEGESSGA--NLSLRPEGSGNTGASQ 111
Db      69 GGGGTTETRTNT-----TATNTVGLGPGSLYTGSVWEKGVNSVGT-- 112
Qy      112 KTESSTGSPVPFDIKAVSISPTVILTWKSNDRASBYK--YVVKHKNENEK--TIVVHQ 168
Db      113 -VTTATPNVRLNLRVAQGNSSIALTWEPDPPDQNSYGVLEYGDDGRATRBTAH- 170
Qy      169 PWCNIT--GLRPATSYVFSITPGIGMETWGDPRVIVKITEPIVSDLRVALTGVRRAIS 226
Db      171 --TNIIVDGLPCLYAFSM----- 188
Qy      227 WSNNGTASCRVLLSISGSHEELQ-----DSRLQVNIISDLKPGVOYNINPYLLQSKTKG 282
Db      189 WVKNGNGNSRETRNATTANPVRKPSGSDQLHLPFL--GGPRW-RTETDLIRLSTA 246
Qy      283 DPLGTEGGLDASNTBESRAGSPPAVHDSLVGPVDPSSGQGRDYEVLVLGLEPSTRYN 342
Db      247 LEMVAEQLRLETOQTPRS-----PVD-----GLGPSGLYT 275
Qy      343 AATYSAQANTBEGQPAIERETNAIOVFDYAVNISATSLITLWKUSDNESSNNTYTKH 402
Db      276 CSVWVEDGVNSSSMRLVYSTAPNVRNLYEAQGNSSIALTWEPDPPDQNSYGYVE 335
Qy      403 VAGETSSNLNVSEPRAVIPGLSSFTYNTICPVYGLDIEGTPGFLQVH----- 451
Db      336 YTDGGR-----GTRSTAHNITVDRL-----EPGLIYVSVWVGKNGINS 377
Qy      452 -----TPPVVDSFRVTVVSTTEIGLAWSHDAE-----SPQWHTQEGAGNSRYEI 498
Db      378 SRETRNATTAPNVRNLIHMETQNSSIALCWEVDPGPQDYTYWVGYGDG--GGETRN 436
Qy      499 TTNQSIILIGLPPGTGYCEIYIPKGNVTEGASRYCAKRTVSAPFDIHVVYTTTEMKL 558

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Db      437 TTNTSVTAERLEPGLTYFSYMAE-KNGARGSRQNVISIVPNAVTSLSKODWTNSTIAL 495
Qy      559 DWKSPD--GASEVYVYHL--VIESKGSNMHTSTYKATITLOGLIGTLNITISPEVDHW 614
Db      496 RMTAPQGPQSSSYYSYWSVWEKMTDPTQSTGTDITLTKLEAGSLVHLTVMAERNEVR 555
Qy      615 GDPSTAQYTPSVSNVIDVSTNTTAATLSWQNF--DDASPTYSCLLIERAGN----- 666
Db      556 GYNSTLTAATAPNEVTDQNTQTKNSYMLMKAPBGDSQLYVYVWQMAKGRPRQD 615
Qy      667 -SSNATGVNVDIGITDATVTELIPGSSYTVVEIPAQVGDGKISLEPRKRSFC--TDPASMA 723
Db      616 PQAMVAVQTSRTNETWYVEALEPGLTYNFTVMAERNDVASTQ---SLCASTYPTDVT 671
Qy      724 SFDEEVVPEKRALVLTCTCPGANAAGPELEVSAGANNATHESSCSENGTEYETVYL 783
Db      672 ITSCVSTAGYVNLIMSCPGGYBAFELEV-----GGQRSGSDRS----- 712
Qy      784 NFSTSYNISTITVTCGKMAAPTRNTCTGTIDPPPDGSPNITSVSHSVKFSGFAS 843
Db      713 -----SCGEAVS-----VLGL----- 723
Qy      844 HGP1KAYAVILTTGEGAPSDVLKTYTDDPKKASDITYYTLIRTEBKRSQSLSEVLK 903
Db      724 -GPARYPATITTT-----IWDGKK-----VVS 744
Qy      904 YEIVDGNBESTLGYNGKLEPLGSRACVAGFTNITFPQNKGLDGAESTVFSRYSDA 963
Db      745 HSNVCHTESA----- 754
Qy      964 VSLPQDDGVICGAVFGCIFGALVITVGGFIEMRKRDADKNNVFSQIKPKKSKL--- 1020
Db      755 -----GVINAGAVGIL--LFLILVGLLIFPLKRRKKK-----QQRPELRLVFS 797
Qy      1021 -----IRVENFEAYRFPKQADNSCGFAEYEDLKLVGISQPKYAAELANRKNRYNVL 1076
Db      798 SPQDIPADFDADHVRKNERDSCGPADREYQQLSLVGHSGQMVASASNNAKNRYNVL 857
Qy      1077 YDIDRVKLS-VQHTSTDDYINANYMFGYHKKDPIATQGPLPNTLAKDWRWVWEKANYAI 1135
Db      858 YDMRSVPLKPRHIEBPGSDYINASFMPGLMSPOEFATQGPLPQTVGDWFLVWEQSHTL 917
Qy      1136 IMLKCYEGRGRTKCEEWYR-SKQADYDITVAMTSEIVLPEMTIRDPYTKNIQTSRSH 1194
Db      918 VMLNLCHEAGRWKCEHWPDLDSQCTGHILNTLVGEVMEWVYRELLILQVEBQKTL 977
Qy      1195 LRQHFHTSWPDHGYDDTDLINFRYLVLDYMKQSPPEPILVHCSAGVGRGTFTAI 1254
Db      978 VRQHYQAMPDHPGPPSPDITLAFWMLRQMLDQMEGGPPIVHCSAGVGRGTTLALDV 1037
Qy      1255 LIYQIENENTVYGIYVDLMARPLMVQTEDOYVFLNQCVDIVRSQ 1302
Db      1038 LLRLQSEGILGIPFSFVRKMKRESRPLMVQTEAOYVFLHQCICGSNSQ 1085

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RESULT 5

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C41214
protein: tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, long splice form precursor
C/Species: Drosophila melanogaster
C/Date: 28-May-1992 #sequence_revision 12-Jun-1992 #text_change 24-Apr-1998
C/Accession: C41214
R/Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, W.
Cell 67, 661-673, 1991
A/Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sube
A/Reference number: A41214; MUID:92034988; PMID:1657401
A/Accession: C41214
A/Molecule type: mRNA
A/Residues: 1-1630 <YAN>
A/Cross-references: GB:M60465
C/Genetic8:
A/Gene: FlyBase:PCP10D
A/Cross-references: FlyBase:FBgn0004370
C/Superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repe

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C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolyase; recept
F:1197-1213/Domain: transmembrane #status predicted <TM>
F:1197-1213/Domain: intracellular #status predicted <INT>
F:1214-1630/Domain: intracellular #status predicted <INT>
F:1255-1515/Domain: protein-tyrosine-phosphatase homology <PMP1>
F:1467/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1473/Binding site: substrate phosphate (Arg) #status predicted

Query Match      14.6%; Score 1028; DB 2; Length 1630;
Best Local Similarity 25.7%; Pred. No. 2,96-49;
Matches 330; Conservative 232; Mismatches 470; Indels 250; Gaps 52;

Qy      119 PSPYFDIKAVSISPTN-VILTKSNDTAASEKYVYKHKE--NEKTTV-VHQPWCNIT 174
Db      405 PLPVNRISINDKNTMTITWEADPASTQDEYRIYVHELETFGNDSTLTTRFTLE 464
Qy      175 GLRATYSVRSITGIGNETMGDPRIYKVTPEIP--VSDLRVALTVGRKAALSMSNG 232
Db      465 SLRPGYVSLSV--QAVKKESENETSIFVYRPSPIEDLSIRMGLN--ISWKS-- 517
Qy      233 TASGRVLESIGSHELTQDSRLQVNIISDLKPGVQYNNIPYLQSNKTKGDPGTGEGLD 292
Db      518 -----DYSKQE-----QIEV-----LVSNGTS 536
Qy      293 ASNTERSRAGSPAPVHDESLVGPVDPSSGQOSRDTEVLVGLPEGRYATVYSQAANG 352
Db      537 DLRT-----QKTESRLVINKLQGAAYELKVA-VSHD 569
Qy      353 TEGQPAIEFRNALIQVDTAVANISATSLTLKRVKDNBSNYYTKIHVAGTDSNL 412
Db      570 LRSPHAYFOAVYNNPNNMTIETVRNSVLYVHSPESGFTYSIRYRTDSQWVRL 629
Qy      413 -NVSEPAVIRGLSSTFYNTVCPLVDIEG--TGGIQTHTPPVPSDFRVTVSTEI 470
Db      630 PSVSTEDADITDKKEXKITIQTAVTSFGVSPVQEVNTTVPNPNSNI-IQLVDSNI 688
Qy      471 GLAASHD--AESFOMH-----IYDGAQNSRVEITTNQSIIGLFPETKYCE 518
Db      689 TLEWPKDEGRVESYILKMPDSNDPGRVQTKVNSNKSADLSTVRVLIGELMPGVQYKFD 748
Qy      519 IVPKPGNTGASATVCNRTYPSAVPDIHV-----YTTTMMLDKMSPD 564
Db      749 IQTYSYGLSGIT-SLVRTPMPLQSDVNVANGKEBERDITLSTYPT-----PQ 798
Qy      565 GASEY-VYHL-----VIESKGSNMHTSTYKATITLOGLIGTLNITISPEVDHWMDP 617
Db      799 SSKFPIYRSGGAEIRDKKLANDT--DRKVTGLVGRILYNI-----VMTVS 848
Qy      618 NSTAQ-----YTRP-----SNVSNIDVSTNTTAATLSWQNFDPASPTYSCLLIE 662
Db      849 GGVASLPIQRQDRLYPEPIQLAHNTITDPEISLRWDLPKGEYNDFOIAYLTADNLL--- 905
Qy      663 KAGNSSNATQVNTDIGITDATVTELIPGSSYTVVEIPAQV--DGKISLEGRKSFCTD- 718
Db      906 -AQNMTRNEI-----TISDLRPHRNTFTVAVRSGTSSVLSNSSLASFITNE 955
Qy      719 --PASMASF-DCEVVPKEPALVLTCTCPGANAAGPELEVSAGANNATHESSCSENGTE 775
Db      956 AVPRVERFHPPTDQPS--INFEMSL-PSEENAGVIRQFIATNINNLTDAGQ---D 1009
Qy      776 YRETVY-----LNFSTSYNISI--TVSCGKMAAPTRN-TCTYGTIDPPPGSPNIT 826
Db      1010 FESSEARFQVINKLARGETVYFKIQAKTALIGG-----PEREVRQMTPLAPRAPATQVVT 1065
Qy      827 SV--SHNSVKYKF--SGFEASHGPIKAYAVILTTGEGAPSA-----DVLKTYTDDFK 875
Db      1066 EYVRSSTTIIQIRFKNYFSDNGQVRYTIIIVADDKAKNAGSGLMPSWLDVQSYSV--WL 1123
Qy      876 KGASDITYYTLIRTEBKRSQSLSEVLKYEIDVNEST---TLGYNGKLEPLGSYRACV 932
Db      1124 PYAIDPYIPFENRSE-----DTTIGTENDNHKIGVCHGPLESGTTIGKV 1170
Qy      933 AGFTNITFPQNKGLDGAESTVFSRYSDAVSLPQDGVICGAVFGCIFGALVITVYGG 992

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Db 1171 RRT-----GADKFTD-TAYPEIQTDDNTSLIVAL--TVPLTIIILVLVT 1214

Qy 993 FIFRRKKR-----KDAK-NNEVSPQIKPKSKXILRVNFEAYRKQAOASNCFAAE 1044

Db 1215 LIYKRRNNCKRTKTQDSRANDMSLPDSVIBQNRPLILKNFAHRLMSADSDFFSSE 1274

Qy 1045 YEDLKLVGISQPKYAAELAEENRGNRYNNVLPLYDISRVKLS-VQTHSTDDYINANMPGY 1103

Db 1275 FEELKRVGRDQPCFTFADLPENRPNKRNFTNLLPYDHSRFLQPVDDDEGSDYINANVPFH 1334

Qy 1104 HSKKDFIATOGPLPNTLKDPMRWMEKKNYAIIMLTKEVQGTKEEYWPSPKQAO-DYG 1162

Db 1335 NSRREFIIVQGPLHSTRDDPMRWCMESNSRAIVMLTRCEKREKCDQYMPNDVYVFAFG 1394

Qy 1163 DITVANTSEIILPEWTIRDPFTVKNIIQTSSEHPLRQFHTSMRPHGVPTDILLINFRYL 1222

Db 1395 DIIVQILNDSHADWMTTEFML--CRGSEORILRHFTTWPDPFGVNPQQLVRFVAF 1452

Qy 1223 RDYMKQSPPEPSPILVHCSAGVGRTGFIAIDRLIYQIENENTVDYVGIYVLDLRRPLMV 1282

Db 1453 RD--RICABQRPIVHCSAGVGRTGFITLDRILQIINTSDYVDIPGIYVARKERVMV 1510

Qy 1283 QTEQYVFLNQCVLDIRSGOKD 1304

Db 1511 QTEQYICIHQCLLAVIBGKEN 1532

RESULT 6

D41214
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, short splice form precursor
C:Species: Drosophila melanogaster
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #ext_change 09-Jul-2004
C:Accession: D41214, A41215
R:Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, W.
Cell 67, 661-673, 1991
A:Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sub
A:Reference number: A41214; MUID:9203498; PMID:1657401
A:Accession: D41214
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1557 <YAN>
R:Titian, S.S.; Teoulfas, P.; Zimm, K.
Cell 67, 675-685, 1991
A:Title: Three receptor-linked protein-tyrosine phosphatases are selectively expressed c
A:Reference number: A41215; MUID:9203498; PMID:1657402
A:Accession: A41215
A:Molecule type: mRNA
A:Residues: 1-904,'L',906-1125,'Q',1126-1165,'YR',1168-1171,'A',1173-1215,'L',1217-1456,
A:Cross-references: GB:M80538; NID:9158644; PIDN:AAA28952.1; PID:9158645
C:Genetics:
A:Gene: FlyBase:FBgn0004370
A:Cross-references: FlyBase:FBgn0004370
C:Superfamily: protein-tyrosine-phosphatase, receptor type 4B; fibronectin type III repe
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept
F:1124-1557/Domain: transmembrane #status predicted <INT>
F:1214-1557/Domain: intracellular #status predicted <INT>
F:1295-1515/Domain: protein-tyrosine-phosphatase homology <PPL>
F:1447/Active site: Cys (phosphotyrosine intermediate) #status predicted
F:1473/Binding site: substrate phosphate (Arg) #status predicted

Query Match 14.6% Score 1026; DB 2: Length 1557;
Best Local Similarity 25.7%; Pred. No.3.5e-49;
Matches 329; Conservative 233; Mismatches 470; Indels 250; Gaps 52;

Qy 119 PPSVFDIAVSIPTN-VILTWKSNDAASEYKVVVKHME--NEKITYV-VHQPWNCNIT 174

Db 405 PUPVNNLSINDDKNTMIITWEADPASTQDEYRIVTHELETFNGDSTLTTRTRFTLE 464

Qy 175 GLRPAIVSITGIGETWGDPRVIVKITEPIL--VSDLRVALLTVGRKAALSWNGNG 232

Db 465 SLLEGRNLSLV-QAVSKKMSNETSIFVVTRPSSPIIEDLKSIRMGILN---ISWKS--- 517

5

Qy 233 TASCRVLLSEIGSHELTQDSRLQVNIISDLKPRQYININPILLOSNKTKGDLCTEGGLD 292

Db 518 -----DVNSKQE-----QYEV-----LYSRNGTS 536

Qy 233 ASNTERSPAGPTAPVHDESLVGPVDPSSGOQSDTEVLVGLRPGFRYNATVYVSOANG 352

Db 537 DLRT-----OKTESRLVINCLOPGAAYELKVA-VSHD 569

Qy 353 TEGQQAIEFTTNAIQVDPVAVNISATSLTLIKVSDNESSNYTKIHVAGSTDSNLT 412

Db 570 LRSEHAFAVQAVNPNPNNMTIEYRSNSVYLVMHSPESGFEYTSIRYRTDSBQWRL 629

Qy 413 -NVSEPRAVITGLRSTSTYNTVTCVYGLDIEG-TPGFLQVHTPPVPSDFRVYVSTTEI 470

Db 630 PSVSTEDITDMTKGKRTTQVNTVSPGVSPVQENVTTPPNPVSNI-IQLVDSRNI 688

Qy 471 GLANSHD--AESFQMH-----ITQEGAGNSHVEITTNOSIIIGLFPETKYCFE 518

Db 689 TLEWPKRPGREVSYILKMWPSDNPGRVQTKVNSKNSADLSTVRVLIGELMPGVQYKFD 748

Qy 519 IVPKGPNTGASRTVCNRTYPSAVFDIHYV-----YTTTBMMLDKSPD 564

Db 749 IQTTSYGLISGIT-SLYPRTPPLIQSDVVYANGKEDEBDRTITLSYRPT-----PQ 798

Qy 565 GASEY-VYHL-----YIESKGSNHTSYDKAITTQGLIPGLTYNTTISPEVDHWVMDP 617

Db 799 SSKKFDIYRPSGDAELRDKKELANDT---DRKTTFGVLPGRLNIT-----VWTVS 848

Qy 618 NSTLQ-----YTRP-----SNVSNIDVSTNTTAATLSQONPDASPTYSCLLIE 662

Db 849 GGVASLPIQRQDRLYPPIQTOLAHNTITDREISLRMLDPKGEVNDPDIAYLTADNLI--- 905

Qy 663 KAGNSNATQVNDIGITDAITVELIPGSSYTYEIFAQVQ--DGKISLEPKGKSTCD- 718

Db 906 -AQMTTTRNEI-----TISDLRPHRYTTTVVRSSTESSVLRSSSPLSASFNTNE 955

Qy 719 --PASMASF-DCEVPEKPAVLKMTCPGANAGFELEVSSGAMNATHLESCESENGTE 775

Db 956 AVFGRVRFPHPTDVQPE--INFEMSL-PESBANGVIRQSIAYTNINNTLDAGMC---D 1009

Qy 776 YRTFVTV-----INFSTYNIISL---TWSCGMAAPTRN-TCTTGITDPPPDGSPNIT 826

Db 1010 FESSEAFGVIKNKKPGETVYFKIQAKTALGFG---PERRYROTMDILAPREPATQVVP 1065

Qy 827 SV--SHNSVYKF--SGFEASHGPRIKAYAVILTTGAGHPSA-----DVLKYTDDPK 875

Db 1066 EYVRSSSTIQIRFRKRYFSDQNGQVMTYITVADAKNAGLEMSWLDVGYSV--WL 1123

Qy 876 KGSADTYVTYLTITEKGRQSLSLEVLYKEIDVGNST--TLGYNGKLEPLGYSYRACY 932

Db 1124 PYAIDPYPPENRSVE-----DFTIGTENCNHKGICNGPLKSGTTIGVAV 1170

Qy 933 AGFTNITFHQNGGLDGAESYVSFSRYSDAVSLPDPQVIGCAVGCIFGALVITYVVG 992

Db 1171 RRT-----GADKFTD-TAYPEIQTDDNTSLIVAL--TVPLTIIILVLVT 1214

Qy 993 FIFRRKKR-----KDAK-NNEVSPQIKPKSKXILRVNFEAYRKQAOASNCFAAE 1044

Db 1215 LIYKRRNNCKRTKTQDSRANDMSLPDSVIBQNRPLILKNFAHRLMSADSDFFSSE 1274

Qy 1045 YEDLKLVGISQPKYAAELAEENRGNRYNNVLPLYDISRVKLS-VQTHSTDDYINANMPGY 1103

Db 1275 FEELKRVGRDQPCFTFADLPENRPNKRNFTNLLPYDHSRFLQPVDDDEGSDYINANVPFH 1334

Qy 1104 HSKKDFIATOGPLPNTLKDPMRWMEKKNYAIIMLTKEVQGTKEEYWPSPKQAO-DYG 1162

Db 1335 NSRREFIIVQGPLHSTRDDPMRWCMESNSRAIVMLTRCEKREKCDQYMPNDVYVFAFG 1394

Qy 1163 DITVANTSEIILPEWTIRDPFTVKNIIQTSSEHPLRQFHTSMRPHGVPTDILLINFRYL 1222

Db 1395 DIIVQILNDSHADWMTTEFML--CRGSEORILRHFTTWPDPFGVNPQQLVRFVAF 1452

Qy 1223 RDYMKQSPPEPSPILVHCSAGVGRTGFIAIDRLIYQIENENTVDYVGIYVLDLRRPLMV 1282

Db 1453 RD--RICAEGRPIVHCSAGVSGSTFTLDRILQIWTSDYVDFIGVIAMRKRKRVMMV 1510
 Qy 1283 QTEQDVYFLNQCVDIVRSQKD 1304
 Db 1511 QTEQDVYFLNQCVDIVRSQKD 1532

RESULT 7

S17671

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 22-Nov-1993 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004

C/Accession: S17671; S40287
 C/Comment: M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.;
 FEBS Lett. 290, 123-130, 1991
 A/Title: Cloning, expression and chromosomal localization of a new putative receptor-like
 A/Reference number: S17669; MUID:9208644; PMID:1655529
 A/Accession: S17671
 A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA
 A/Residues: 1-583 <GB>
 A/Cross-references: UNIPROT:Q64497; EMBL:X58289

R/Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993

A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A/Reference number: S40280

A/Accession: S40287
 A/Molecule type: mRNA

A/Residues: 377-483, 'T', 485-486 <HEN>

A/Cross-references: EMBL:223056; NID:9438149; PIDN:CA060591.1; PID:9438150

C/Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot
 F/311-536/Domain: protein-tyrosine-phosphatase homology <FR>
 F/468/Active site: Cys (phosphocysteine intermediate) #status predicted

F/494/Binding site: substrate phosphate (Arg) #status predicted

Query Match 14.0%; Score 981.5; DB 2; Length 583;
 Best Local Similarity 39.0%; Pred. No. 2.4e-47;

Matches 226; Conservative 102; Mismatches 191; Indels 61; Gaps 15;

Qy 789 YNISITVSCGKMAAPNTCTTITDPPPGSPNI-----TSVSHSVK-VKPSGF 840
 Db 5 YLVSITKQVAGMTSEVEDSTITMIDRPQ--PPIHVNKVDLISKSNFTVNCWF 62

Qy 841 EASGPIKAVVITTG-----EAGPSADVLTYYDPFKGASDTTYTILRTBEK 892
 Db 63 SDTGAAGYFAVVVREADSMDELKPEQHPPLSYLYEHNNASIRVYQTNV--FASKCAES 120

Qy 893 GRSQSLSEVLYKEIDVGNSTTLG-----YNGKLEPLGSRACVAFNTITPHQ 943
 Db 121 PDSSSKS---FNITKGLHMDSLGKCDPSQKFCDEGLLPHTVIRISIRAFQIF---- 172

Qy 944 NKGLIDAGSEVVSFSRYSDAVSLPDP--GVICGAVFCIFGALVITVVGFIWKR--K 999
 Db 173 DEDKEFTKPLVSDTPFSMPITTESEPLFGVIEGVSAGFLIGLVLVAVAFICQKQASH 232

Qy 1000 RKDAKNNVFSQIKP-----KSKLIRVENFAVYRKQADNSCGFAEYE 1046
 Db 233 SREPSARLSIRRRPLSVHLNLGQKGRKTSCEPIKIQFGHFMRKQADSNVLSKYE 292

Qy 1047 DLKLVGASQPKAELNENGRNRYNNVLPYDISRVKLS-VQTHSTDDYINANYMPGHS 1105
 Db 293 DLKVGASQSCDILLPENRGRNRYNNVLPYDASRVKLSVDDPCSYINASTYIPGNF 352

Qy 1106 KKDIATQGPLLNTLKDFWVWVWKNVYAIIMLTCKVEQGRTKCEYVPSQK-AQDYGI 1164
 Db 353 RREVIATQGPLRGTKDDFWKVAEONVANIYVATGCVCEKGRVCKDHVVPADQDPLYYGDL 412

Qy 1165 TVANTSEVLEBMTITRDVTVKNIQTSESHPL-RQHFPSWPDHGVPTDILLINFRILYR 1223
 Db 413 ILQVNSVSLPEWMTIRFVKISEQDLAHLRIHFRHYVWPDHGVPTDILLIOFVRTVR 472

Qy 1224 DYKQSPPESEILVHCSAGVSGSTFTALDELILQIWTSDYVDFIGVIAMRKRKRVMMV 1283
 Db 473 DYINRSPGAGSVVHCSAGVSGSTFTALDELILQIWTSDYVDFIGVIAMRKRKRVMMV 532
 Qy 1284 TEDQVYFLNQCVDIVRSQKDLIYQNTAMTITEN 1323
 Db 533 TECQVYFLNQCVDIVRSQKDLIYQNTAMTITEN 568

RESULT 8

A55148

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
 N/Alternate names: OST-PP; osteosticlicular protein-tyrosine-phosphatase

C/Species: Rattus norvegicus (Norway rat)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: A55148
 R/Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.

J. Biol. Chem. 269, 30659-30667, 1994

A/Title: Identification of a hormonally regulated protein tyrosine phosphatase associated
 A/Reference number: A55148; MUID:95074080; PMID:7527035

A/Accession: A55148
 A/Status: not compared with conceptual translation

A/Molecule type: mRNA
 A/Residues: 1-1711 <MAU>

A/Cross-references: GB:136884

C/Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosi
 C/Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III rep
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/119-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MA
 F/1174-1398/Domain: protein-tyrosine-phosphatase homology <PP1>
 F/1350/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 13.6%; Score 957.5; DB 1; Length 1711;
 Best Local Similarity 24.5%; Pred. No. 2.8e-45;

Matches 383; Conservative 227; Mismatches 524; Indels 431; Gaps 72;

Qy 22 PLILL--ILRIGQL-----CA--GMP-----SPIDPSVAT-----VATGEN 56
 Db 3 PLILLALMLQGLAADDACSLIGSPDRQGGPLLSVNSHGKSTSLFLSVVAELG 62

Qy 57 GITQISSTAESFHKQNGTGP--QVEHTNSEDE-ESSGANDS-----LRTPEGS 103
 Db 63 GF-----DYALSLRVDSSGSEGGQLQAHNTSEFFHGLVPSRYQLKLVLPQGNV 118

Qy 104 NGTDGASQKTPSSSTGSPVPEDIKAVSI-SPTNVILTWKSNDAASEYKVVYKHQENEXT 162
 Db 119 TIT-----LTARFAPTVVVGILQLHSAGSPARLEASWSDAPGDOSYQLLYH-LLESQ-T 170

Qy 163 ITTVHQPWCNT-----GLRPATSVYFSTITGIGNETMGDRVIVKI-----TEP 207
 Db 171 LA-----CNVSPDPLYSFGDLRPGQVLEVT-----TWAGSLHAATSLIOWTEP 218

Qy 208 IPVSDLEVALTGVAKALMSNGNGTASCRVLLESIGSHELTODSRLOVN---ISDLKP 264
 Db 219 VPPHMLALRALGTSLQAFNMSSEGATSFHMLMLDLGNTTAVIIGQVSTHFFHLSP 278

Qy 265 GVQVYNIPYLIQSNKTVG--DPLGTE----- 288
 Db 279 G-----TPHELIKASAGPHQIWPASRAPEWTYPSYPSDVLVPLRNELMSWKAGLGARD 333

Qy 289 -----GGIDASNT-----EKSRA--GAPTPAVHD-----ESLVGVD-----PSGQ 323
 Db 334 GYVLKLSGPEWSTITLPEBCNAVPGPLPFGHTTLQKVLAGDYDMWEGSTLAEASAA 393

Qy 324 QSRD--TEVLLVGLF-----PGRYNATVYSQAANGTEGQPOALEFTNALQVDPVAVN 376
 Db 394 LPREVPARLMLDLAEASKQGR--ALIVSDAPSLG-----N 431

Qy 377 ISATSLTLIMKVDNNESSNTYKIHVAGETDSSNLVSEPRAVIPGLRSTFPNITVCP 436
 Db 432 ISVPS-----GAT-----HVIFCGLVPGAHYVDIAS 458


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Db      986 VSTLMRSSA--PISASYOTLT-----APPGKVDYFQPSDVQ-----1019
Qy      594 QGLIPGTLNITISPEVDHW-----GDNSTRAQYTRPBNVSNIDVSTTTAATLSMWFND 649
Db      1020 ---PG-----EVTFEWSLEPAEQHGPIDYFR-----ITCQAD 1049
Qy      650 DASPTYSYCLLIEKAGNSNATQVVTDIGIDATVTELEIPGSSYVEIFAQVGDGKISLE 709
Db      1050 DAADVSSIEFPV-----NATQ-----GKIDGLVPGNHIIYFRQAQSAAGY-----1089
Qy      710 PGRKSFCTDPASMASFCEVVPKEPALVLKWTCPGANAGELEVSQGMANNATHLES 769
Db      1090 -----GAERE-----HIQ---1097
Qy      770 SENGREYRETVYLNFTSYNISTITVSCGMAAPTRNTCTGTITDPPPGSPNITSVS 829
Db      1098 -----TWPIIAPVPPESTVPLEVS 1117
Qy      830 HNSVVKFS-----GFEASHGPIKAYAVILT--TGEAGH---PS-ADVLKYT---YDDE 874
Db      1118 RTSSTIEISFPGQYFSNNAHGWASTIIIAEDVNGKIASGLEMPQDQATVWMLPYQ-- 1175
Qy      875 KKASDITYVYLIRTEERKRSQSLEVLKYEIDVGN-ESTTLGYNGKLEPLGSTRACVA 933
Db      1176 ---AIEPYNPFL--TSNGSRKSSL-EASHLITIGTANCDKHQAGYCNGLPAGTYRIKIR 1229
Qy      934 GFTNTTFHPQKGLIDAGSYVSFSRYSDAVSLPQ-DGVCICGANFGCIGALVIVTYGG 992
Db      1230 AFTD-----EDKFTDVTYSSPTTERSDTVIAATVSAVLAVALVAVV-- 1273
Qy      993 FIFRRKKRDKAKNNNEVSFOIKPKKSKL-----IRVENFEAYFEKQOASNGCFA 1042
Db      1274 ---YQHRCQOLIRASKLARQDELALPEGITTRNVVHKDPESEHRIKMSADDFRS 1330
Qy      1043 EYEDLKLKLVGISQPKYAAELAEENRKNRYNNVLPDISRVKLS--VQTHSTDDYINANTP 1101
Db      1331 EEPFELKLVGRDQACSFAFLPCNRPKNRFNTLLPYDHSRFLQDPVDDDGSIYINANTP 1390
Qy      1102 GYHKKDILATQPLPNTLKPWRVWMEKNVYAIIMLKCYEGQGTKEBWP-SKQAD 1160
Db      1391 GHNSPREFTVTOGPRHSTRFEERWCMESNSRAIYMLTRCFEKREKDDQYTPVDRVAMF 1450
Qy      1161 YGDIYVANTSEIIVPEWTRIDFTVKNIQTSSESHPLRQPHFTSMPHGVPDITDLINFRY 1220
Db      1451 YGDIKVOQLIDITHHDSISEFMS--RNCESRIKRNHFTFTWPRGPBEPLSLVRVR 1508
Qy      1221 LVDRYMKSPSPSPILVHCSAGVGTGFIAIDRLIYOIENENTVAVYGIYDLMAHPL 1280
Db      1509 AFRDVI--GDMRPIIIVHCSAGVGRSGFIALDRILQIHKSDDYDIFGIYAMKERVF 1566
Qy      1281 MVQREDQVYFLNQCVLDIRSOKSKVDLI-----YQNTAMTYENLAPVYTFG 1330
Db      1567 MVQEQQVYCIHQCLAVLEGEKHLADSLHLANDGYEVT--KTYLEROPQTMG 1620

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RESULT 10

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B49502 protein-tyrosine-phosphatase (BC 3.1.3.48) receptor type 4E, splice form B precursor - f
C/Species: Drosophila melanogaster
C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: B49502
R/Oon: S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 266, 23964-23971, 1993
A/Title: Alternative splicing in a novel tyrosine phosphatase gene (DPT4E) of Drosophila
A/Reference number: A49502; MUID:94043220; PMID:8226938
A/Accession: B49502
A/Molecule type: mRNA
A/Residues: 1-1615 <OON>
A/Cross-references: UNIPROT:Q9MAF5; GB:U20894
C/Genetics:
A/Gene: FlyBase:Ptp4E
A/Cross-references: FlyBase:FBgn0004368
A/Introns: 1605/3

```

C/Superfamily: protein-tyrosine-phosphatase, receptor type 4E, fibronectin type III repe
 C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept
 F:1254-1270/Domain: transmembrane #status predicted <TM>
 F:1271-1615/Domain: intracellular #status predicted <INT>
 F:1353-1573/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:1525/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1531/Binding site: substrate phosphate (Arg) #status predicted

Query Match 13.5%; Score 949; DB 2; Length 1615;
 Best local similarity 24.5%; Pred. No. 7.8e-45;
 Matches 345; Conservative 177; Mismatches 438; Indels 448; Gaps 54;

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Qy      67 SFHQ-NGTGR-----QVETNTSE-----DDESSGAND-- 94
Db      469 SYHQTNASRPAPPPVAASQITNTLETYLDSLNGRLIAVQALSKVANSASIT 528
Qy      95 -----SLRPEQG-----SNGTDGASQKTPSSTG-----118
Db      529 RYTRPAAPLIQELSIDGLMLSWRSDVNSRQDREYEVHQNCTREERTMATNETSLTIH 588
Qy      119 ---PSVPDIKAVSIS-----PTN-----VILTKNSDITAS 147
Db      589 YLHSGGEVAVHAIHSGVRSEPHSYFOAVPPKPQNTLTQVHTNLVLMQAPE--GS 646
Qy      148 EY-KYVVGKMKENKTIIVVHPQCNITGLAP-----ATSYVPSI--TPGIGNETW 195
Db      647 DFEYVYVRKD-----ASPWQRISGLHENEARIKDMHGERYLVQVNTVSGVES- 697
Qy      196 GDRVIKYTEPIPVSDRLVALTGVRKAALSWSNNGTASC-----RYLLESI 243
Db      698 PHLPLANTMPQPVSNV-VPLVDSRLNLTLEMPRPDGHVDEYTLKMPETDEEDREYFKNV 756
Qy      244 GSHBELQDSSLQVNIISDLKGVQVYNNPVLQSNKTKGDLGEGGLDANTERSRAGS 303
Db      757 TQLEDSLSPS-VRIPIEDLSFGQYR-----EQVASSNGRSQTHLSRTFM 803
Qy      304 PTAPEHDSILGVPDPSSGQSRDTEVLVLGLAP-----GTRYNATVYSQANGTEGCPQA 359
Db      804 PL-IQSVFIA---NAGHEQGDDEITLSTYTPPADSTRFDLYRFEM---GDP-- 849
Qy      360 IEFRTNALQVDPVAVNISATSLTLWKVSDNESSNTYKIIVAGETDSSNLVSEPPA 419
Db      850 -----TIKQEKLANDT-----ERKL 865
Qy      420 VILPGRSTFYNTICPVLDIGETPGELQYHTRPVPVSDPRVTVYSTTEIGLAWSSHDA 479
Db      866 SPSGLTPGKLVNVTWTVSSGGVASLPQVRVYRHLPLPSIDKAIQVAAERITLMTAPAG 925
Qy      480 E-----SPQMHTQEGAGNSRVEITTNOSIIIGLFGPGKYCFEIVPKGPN--GTEGASRT 533
Db      926 EYTPPELOYSADDEAPQLQONVTKNTEITLQGLRPYHNHYFTVYVNSGSIQGTDFADVS 985
Qy      534 VCNRTVPASVEDIHVVYVTTTMMWLDWKSPPGASEYVHVLIESKHGNSHTSTYDKAITL 593
Db      986 VSTLMRSSA--PISASYOTLT-----APPGKVDYFQPSDVQ-----1019
Qy      594 QGLIPGTLNITISPEVDHW-----GDNSTRAQYTRPBNVSNIDVSTTTAATLSMWFND 649
Db      1020 ---PG-----EVTFEWSLEPAEQHGPIDYFR-----ITCQAD 1049
Qy      650 DASPTYSYCLLIEKAGNSNATQVVTDIGIDATVTELEIPGSSYVEIFAQVGDGKISLE 709
Db      1050 DAADVSSIEFPV-----NATQ-----GKIDGLVPGNHIIYFRQAQSAAGY-----1089
Qy      710 PGRKSFCTDPASMASFCEVVPKEPALVLKWTCPGANAGELEVSQGMANNATHLES 769
Db      1090 -----GAERE-----HIQ---1097
Qy      770 SENGREYRETVYLNFTSYNISTITVSCGMAAPTRNTCTGTITDPPPGSPNITSVS 829
Db      1098 -----TWPIIAPVPPESTVPLEVS 1117
Qy      830 HNSVVKFS-----GFEASHGPIKAYAVILT--TGEAGH---PS-ADVLKYT---YDDE 874

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Db      1118 RTSSTIETISFROGYFNSAHGVNRSYTIITIAEDVKIASGLGEMPSMDQVQVITWLYQ-- 1175
Qy      875 KKGSADYVYVYLLRTEKGRSOSISEVLKYEIDVGN-ESTTLGYNKGKLEPLGSRACVA 933
Db      1176 ---AIEEYNNPPL--TSNGSRKSSSL-EAEHLTITGANCDDKHQAGYCNCPPLAGTYYIKIR 1229
Qy      934 GFTNITFHPONKGLIDAESEVSFSRSDAVSLPQ-DPGVICAGVGCFCGALVITVVG 992
Db      1230 AFTD-----EDKFDITYSSPITERSSTIVVAATVSAVLVAVLVV-- 1273
Qy      993 FIFWRKKRKAANKNEVSFSQIKPKSKL-----IRVENFEAVFKKQADSNCGFA 1042
Db      1274 ---YQHRCOLIRRASKLARMODELALPEGYITPMPRYAVKQFSSHYRIMSADSPFRS 1330
Qy      1043 EEEYEDLTVGISQPKYAELENRGNKRYNNVLPYDISRKLS-VQTHSTDDVYNNVMP 1101
Db      1331 EEEBELKHVRDQACSPANLPCRKPKRRFTNLPYDHSRFLQPVDDDDGSDIYNNVMP 1390
Qy      1102 GHNSKDFLATQGPLPNTLKDFFRWVWEKNVVAIIMLKCEQGRKCEYMP-SKQAD 1160
Db      1391 GHNSPREFIVTQGPFSHSTREEFWRCMESNSRAIVMLTQCFEKGREKCDQVMPVDRVAMF 1450
Qy      1161 YGDIYAMNSEIYLPMTITRDFTVYKNIQISEHPLAQFPTSPDHGVDTTDLINFRY 1220
Db      1451 YGDIKQQLIITHYHWSISEFWVS--RNCESKIMHFHTTWPDPGVEPEPLSLVRFVR 1508
Qy      1221 LVADYKQSPESPPIIVHSGAGVGTGTFLAIDRLIYQIENENYDVVYIVDLMHNPRL 1280
Db      1509 AFRDVL--GTDMPPIIVHSGAGVGTGTFLAIDRLIYQIENENYDVVYIVDLMHNPRL 1566
Qy      1281 MOTEQYVFLNOCVLDIYRSQKSKVD 1308
Db      1567 MOTEQYVFLNOCVLDIYRSQKSKVD 1594

RESULT 11
A:56178
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
M:Alternate names: protein-tyrosine-phosphatase BPTP-2
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56178; S12052; B44929
R:Pullido, R.; Kruenger, N.X.; Serra-Pages, C.; Saito, H.; Screuli, M.
J. Biol. Chem. 270, 6722-6728, 1995
A:Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.
A:Reference number: A56178; MUID:95204468; PMID:7896816
A:Accession: A56178
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1912 <PUL>
A:Cross-references: UNIPROT:P23468; GB:L38929; NID:9755652; PIDN:AAC41749.1; PID:9755653
R:Kruenger, N.X.; Screuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases.
A:Reference number: S12049; MUID:91006018; PMID:2170109
A:Accession: S12052
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 390-1912 <KRUY>
A:Cross-references: GB:X54133; NID:935789; PIDN:CAA38068.1; PID:935790
R:Adachi, M.; Sekiya, M.; Ariyama, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yada
Cancer Res. 52, 737-740, 1992
A:Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A:Reference number: A4929; MUID:92119637; PMID:1370651
A:Accession: B44929
A:Molecule type: mRNA
A:Residues: 1756-1804 'C', 1806-1845 <ADA>
A:Cross-references: GB:S78086; NID:9243545; PIDN:AAB21147.1; PID:9243546
R:Experimental source: pre-B cell NALM-6
A:Note: Sequence extracted from NCBI backbone (NCBIIN:78086, NCBIIP:78087)

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A:Note: the authors did not report the entire codon for residue 90
C:Genetics:
A:Gene: GDB:PTPRD
A:Cross-references: GDB:131384; OMIM:601598
A:Map position: 9p24-9p24
C:Superfamily: leukocyte antigen-related protein, fibronectin type III repeat homology, 3
ogy
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane p
F:38-100/Domain: Immunoglobulin homology <IMM1>
F:140-209/Domain: Immunoglobulin homology <IMM2>
F:250-304/Domain: Immunoglobulin homology <IMM3>
F:711-811/Domain: fibronectin type III repeat homology <3PR>
F:1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1553/Active site: protein-tyrosine-phosphatase homology <PTP2>
F:1553/Binding site: Cys (phosphocysteine intermediate) #status predicted
F:1844/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match      12.5%  Score 879; DB 2; Length 1912;
Best Local Similarity 24.3%; Pred. No. 8,56-41;
Matches 375; Conservative 209; Mismatches 560; Indels 400; Gaps 67;

Qy      14 SPGLRMALPLLLRLGLQLCAGTSPPIPDPSVATVATGNGITQISSSTASFRKNG 73
Db      212 SAGTRYSAPAVLYRELREVRVPRRS-IPPTNHEIMPGGSVNTTVA----- 259
Qy      74 TGTPO-----VETNSDEGSSGAND-SLRTPEGNGT-----DGASQKP 114
Db      260 VGSFMPYVKMMLGAEDLTPEBDMPIGRNVLELNDVROSANYTCVAMSTLGIVIAIAQITV 319
Qy      115 SSTSPSPFDIKAVSISPTVITLWKSNDTAASEYKVVGHKME-----KITTVHQPV 170
Db      320 KAL-PKPRGPVTVTSTRTATISITLWDSGNPEPVSY-YIIOKKNSBELYKEIDGVAITR 377
Qy      171 CNITGLRPATSYVFSITPGLIGNETWGDPR--VIKVITEPIVPS--DLRYALTGVKKAAL 225
Db      378 YSVAGLSPPSYDYERRVY-ANNVIGRGPSEPVLTQISEQAPSSAPPDVQARMLSSTIIV 436
Qy      226 SW--SNGNGTASGRVLSEISGHEELTQSRQVN-----ISLKGVOY 268
Db      437 QWKEEPEPNQIQ-----GRRVYVYMDPTGVNMMKKNVADAQITTTIGLVLOKXY 488
Qy      269 NINPYLLQSNKTKGDDPLTEGGLDASNTERSRAGSPAPVHDESLGVDPSSGQGSRPD 328
Db      489 SVKVLAFTS-----IG-DGLSSDIQVITQGVGGQLNFRFA-----EPES-----ET 530
Qy      329 EVLL-----VGLPEGRY-----NATVYSQAANGTE 354
Db      531 STILLSWTPPRSDTIANYELVYKDGEGEORITIEPGTSYRLQGLKPNLSLYFRLLA---A 587
Qy      355 GQPOALIEFRINAIQV-----FDYAVNVISATSLTLWK-----VSDNESSNNTY 399
Db      588 RSPQGLGASIAEISATMOSKSPAPODDISCSPPSSTILVSNQPPVEKQGITTEYSI 647
Qy      400 K-IHVAGETDSNLNVSEPR--RAVIPGLRSTFNITVCVGLDIEGTPGLQV----- 450
Db      648 KYTAVDGEDDKPHEILIGIPSDTTKYLLFQLEKMTVEYRITV-TANDVGRGPESSLGLRT 706
Qy      451 --HTPPVPVSDPRVYVYVSTTBIGLAMS-----HDAESFQMHITQEGAGNSR----- 495
Db      707 NEDVPGPRKQVEAVENSTSVKSWRSVVPKQHQIRGQVHNHYVRMENGEPKQOPMLK 766
Qy      496 -----VELTTQSIILIGLFPQTKYCFEIVPKGPNTEGASRTVCNRTVSAVDP 545
Db      767 DWVLADAQWEPDTEHMDIISGLQPEISYSLTVAITTKG-DGA-----RSKELVST 819
Qy      546 IHVY-----YVTTTMM--WLDWKP----- 563
Db      820 TGAIVPGKPLVINHQMTALIQMHPVDTPFGLQYRLKFGKMDMEPLTTLTLESEKDH 879
Qy      564 -----DGASRYVHLVIESGSGNSHSTYKATITLQGLPGLTLYNTITSPEDVHWGD 616

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Db 880 FTATDIHKGAS-YVFRLSARKVGFGEEMV--KEISIEEVP-----TGFPMIASEG- 929
 Qy 617 PNSTAOYTRSNVSNIDVSTTTTAATLSKQNFDDASPTYSCLILEKAGNSNATQVYTD 676
 Db 930 -----TSTISVQLSWQ-----PP-----VLAENNGIITKYLTLRYD 960
 Qy 677 IGI-----TDAVTTELIPGSSYVEIFAQVGDGKISLEGRKS-----FCTDP 719
 Db 961 INIPLMEQLIVADDTMLTLGKLPDTTYVVKRAHNSK-----FGPISPVQFTLP 1015
 Qy 720 ASMA---SPDCEVPEKPEALVLTCTCPGANAGLELVSSGAMNATHLESCESENGTEY 776
 Db 1016 VDOVFANFHYKAMK-TSVLLSWEIPEANYSAMPFKI---LYDDGKMEVEV---DSRAT 1068
 Qy 777 RTEVTYNFSTSYNIST---TVSCGMAAFTNTCTGTIDPPPPGSPNITSVNSV 833
 Db 1069 OKLIVNKPEKSYFVLNRGNSAGLOHRYTAKTADVLTAKAFIQTNLDMG---I 1124
 Qy 834 KYKFGSEASHGPIKAYAVIL-----TTGEAGHPSADVLKTYDDPKKASDTYVYLIR 888
 Db 1125 TVQLPEPANEN-IKGYITIIIVLKSRGKIKFWESPDMEDELKEISRK-----R 1178
 Qy 889 TEKGRSQSLSEVLKYEIDVGNESITLG---YNGKLEPLGSYRACVAGFTNITPHQNK 945
 Db 1179 SIRYGREVELKPYIAAHFDVLPTEFTLGDDKH-----GGFT-----NK 1217
 Qy 946 GLIDGASYSYF-----SRYS-D-AVSLRQDP-----GYI---CGAVFG 979
 Db 1218 QLOSGOE-YVFFVLAVMEHESKMYATSPYSDPVAUSDLDQPIITDEEGILVWGPVLA 1276
 Qy 980 CIFGALVTVVGGFIFPRKCKKADKNNEVSPSQIK-----PKSKLIRVENFEA----- 1028
 Db 1277 VVFLICIVAI---LYKRAESDSKRSIIPNNKEIPSHIPTPVELRLINFTQPGMAS 1333
 Qy 1029 -----YFKKQADNSCGFAEYEDLKLVGISQPKYAEALENGRNRYNVLKY 1077
 Db 1334 HPPILELADHIERLKANDELKFSQYESID-PGQGFTEHSHNLVANKPKNRYANVAY 1392
 Qy 1078 DISYVKS-VQTHSTDIYANANMPGYSKDDFIATGCPRLNTLKDTPFRMWEKNVAIL 1136
 Db 1393 DHSGVLLSALIEGRISDYVANNYIDGRKONAYIATQSLPETGDFRMLMEGRSATV 1452
 Qy 1137 MLTCVGEQGRKCEYMPKSOADYGDITVAMTSEIVLPEWTIRDFTVKNIQTSSEHPLR 1196
 Db 1453 MMTLERSKVKCCQYPSRGTETHGLVQVTLTLVELATYCVATFPALYKNGSSEKKEVR 1512
 Qy 1197 QFHTSPWDHGVPTDILLINFRYLVDYMKQSPPEP-PILVHCSAGVGTGTFPIADRL 1255
 Db 1513 QFGTAMPDHGVPHPTPLAF---LRRVKTCPNPDGAPVHCSAGVGTGTFVIDAM 1569
 Qy 1256 IYQIENENTVDYVIGYVDLRMHRPLMOTEDQYVFLNQCVLDIV 1299
 Db 1570 LERIKHEKTYDIYGHVTLMRQRYMYQTEDEQYIFIDALLEAV 1613

RESULT 12
 T14328
 protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type, Gmcl precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T14328
 R/Wright, M.B., Hugo, C., Seifert, R., Distche, C.M., Bowen-Pope, D.F.
 J. Biol. Chem. 273, 23929-23937, 1998
 A/Title: Proliferating and migrating mesangial cells responding to injury express a novel
 A/Reference number: Z17986; MUID:98395110; PMID:9727007
 A/Accession: T14328
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Reidues: 1-2302 <MRI>
 A/Cross-references: UNIPROT:O88488; EMBL:AF063249; NID:G3300095; PID:G3300096; PIDN:AAC3
 A/Experimental source: strain wistar
 C/Genetics:
 A/Note: PTRRO

C/Keywords: phosphoric monoester hydrolase
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/19-2302/Product: protein-tyrosine phosphatase receptor type, Gmcl #status predicted <M

Query Match 12.3%; Score 864; DB 2; Length 2302;
 Best Local Similarity 23.5%; Pred. No. 7.9e-40;
 Matches 405; Conservative 216; Mismatches 533; Indels 568; Gaps 77;

Qy 87 GESSGANDS---LRTPEGNGNGTDGASQKTPSSGPEVPVDIKAVISPTNVLITW----- 139
 Db 648 GESSISENDIFVATPED-----EPES---SPQ-DVQYGVSPBELRKMSPE 692
 Qy 140 KSNDDASERYVYVHK---MENKTIIVVHQPWCNITGLRPAATSYVSTP---GIG 191
 Db 693 KPNGLIIIA-YEVLQNADLTFVKNITSTTDII-----ISDLKPYTLNIGISYTRLGHG 745
 Qy 192 NETWG--DPRVYKITEPIP--VSDLRVALTGKAAALMSNGNG-TASCVLLSEISGSH 246
 Db 746 NQSSSLSVSTSETPVPSAENITVKNISSGEIEISFLPRSPNGIIOKTYIYKRNSH 805
 Qy 247 BELT-QDSRLQVNSDLKPGVQVNNIPYLLQSNKTKGDPITGEGGLDASNTERRAGSP 305
 Db 806 EARTINTTSLQITGGLKTYHYIE--VSATLKGE--GIRSRPISLIEEDAPDSPP 860
 Qy 306 APVDESLVG-----PVDP-----SSGQOSRDEVLV--GLERQTR 340
 Db 861 QNFSVKQLSGVTWLSQWPLEPENGILLYTVYWDKSLRAINATBASLVLDLYNVD 920
 Qy 341 YNATVISOANGT-EGOPQAIERTNAIQVF---DYTAVNISATSLTLW----- 386
 Db 921 YGACVTAFTSTFGDNARSSIIINFRTPEGEPSDPENDVHYVLLSSSSIIILFWTPPVKENG 980
 Qy 387 -----KYSDNSSS----- 395
 Db 981 IQYVSVYQNTSGTFVQNFLLQVTKESDNTVARSARILRAISYTFWLTASTSVNGN 1040
 Qy 396 -----NYTK-----IHVAGETDS-----NLNVSEPR 418
 Db 1041 KSSDIHVTYDQDIPBEPVGNLTFESISSTAHSMWEPSPQPNGLVYYLSLNTQSPPR 1100
 Qy 419 AVTP-----GLRSTFYNTVCVPLGDIESTPGF-----IQVH-----T 452
 Db 1101 HMIPPLTYENSIDFDLLEKTYDIFKITP-----STEGKSESYTTQLHKTEDVPT 1155
 Qy 453 PPVPSVDFRTVYVSTTEIGLAMS---SHDASFGMHTQSGAGSRVEITNOSIIIGL 509
 Db 1156 PPI-INTEK--NLSSTILSMWDPPLKPNGAILGLHLLQGPANHTFVTSGNHIVLEEL 1212
 Qy 510 FPGTKYCFEIVPKGPNGTGASRTVCNRTVPSAVF---DIHVYVYTTTEMLDMK-SP- 563
 Db 1213 SPFTLVFFFAAKRTMKGL-GPSSILFPYTDASAPLAPQNLTLINTYSDFWLWMSPL 1271
 Qy 564 DGASEVYHVLVESKHSNHTSYDKAIT-----LQGLPGTLVNTTISPEVDHWGD 616
 Db 1272 PGGIYKYVSFKI---HEHETDVFYKNISGLQTDKLEGLEPVSYSVASAFKVGNGN 1328
 Qy 617 PMS-----TAQYTRPSNVSNID-VSTNTTAATLSMWFDDASPTYSYCL--LIEKAGNS 668
 Db 1329 QYSNVVEFTTQESVPEAVNRIBECARWQSVSWM---DPRKNTGIIIMHTIVGNS- 1384
 Qy 669 NATQVMTDIGTDA--TVTELIPEGSSYVEIFAQVGDGKISLEGRKSPCTDPASMASFD 726
 Db 1385 -----TKVSRDPTTYFTKLDPMTSYVFEVRASTSG-----BGNSRC-DISTLP--- 1429
 Qy 727 CEVVPKEPALV-----LMTCP----- 743
 Db 1430 -ETVPSAPTVNAFNGVOSTATLTWTKPDITFGFYQVYKITTLQRAQKCEWEEBECIEH 1488
 Qy 744 -----PG----- 745
 Db 1489 QKDQYLYEANTQETELTGLKFRMYRPOVAASTNVGYSNASEWISTQTLPEPPDPGPPENV 1548
 Qy 746 ---ANAGFELEVSAGANN-----NATHLESCESENGTEYRTE 779

Qy	1046	EKLVLGISOQKVAEELAEENGKRNYNVLPEYDISPKVL--SVQHSISDDVYINANMYMGXH	1104
Db	915	BEKLTLGIDLPHPAANDLPANCKNRKYNILPEYDSRVLVLSMNEEGADIIINAYITGIN	974
Qy	1105	SKDPIATQGBLPNTLKDPMRWMEKNVAYALIMLTCKVEQGRTKCEEYWP--SKQADQYGD	1163
Db	975	SPQSYITQGBLPETRNDFMFMVTLQQSKQILITMLTQCNEKRRVACDHWPPTPEIRIYGD	1034
Qy	1164	ITVAMTEIYVLEKTIIDPEYKNIQTSSESHLRQPHFTSWRDHVP--DTTDLILNRYL	1221
Db	1035	ITVAMISEEODDACHFRIN--YADMQDVMEFNTPAMPDHSVPTANAAESTLQGVHM	1092
Qy	1222	VRDYMKQSPESPILVHCSAGVGRGTGFIALDRILYQIENENTVDVYGIAYDLERMRPLM	1281
Db	1093	VROQATKS--KGPMLIHCSAGVGRGTGFIALDRILQHRDHEFDIIGLVSEMSYSYMSM	1150
Qy	1282	VQTEQYVFLNQCV--LDIVASQKDSKVDLYQNTT	1315
Db	1151	VQTEQYVIFHQCVQLMMMKRQQFCISDIVEYEVNS	1186

RESULT 14

A53661 protein-tyrosine-phosphatase (BC 3.1.3.48), receptor type O precursor - rabbit

N:Alternate names: GLEPP; glomerular epithelial protein 1

N:Contains: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphatase C/Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 07-Oct-1994 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C:Accession: A53661

R:Thomas, F.E.; Wharram, B.L.; Goyal, M.; Wiggins, J.E.; Holzman, L.B.; Wiggins, R.C. J. Biol. Chem. 269, 19953-19962, 1994

A:Title: GLEPP, a renal glomerular epithelial cell (podocyte) membrane protein-tyrosine A:Reference number: A53661; MUID:94327545; PMID:7519601

A:Accession: A53661

A:Molecule type: mRNA

A:Residues: 1-1187 <THO>

A:Cross-references: UNIPROT:Q28613; GB:U09490; NID:952941; PID:AAA61709.1; PID:952941212

A>Note: authors translated the codon GGC for residue 1101 as Gln

C:Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repeat C:Keywords: glycoprotein; kidney; phosphoprotein; phosphoric monoester hydrolase; receptor F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-818/Domain: extracellular #status predicted <EXT>

F:30-115/Domain: fibronectin type III repeat homology #status atypical <FN3A>

F:316-209/Domain: fibronectin type III repeat homology #status atypical <FN3B>

F:338-415/Domain: fibronectin type III repeat homology #status atypical <FN3D>

F:431-519/Domain: fibronectin type III repeat homology <FN3E>

F:528-625/Domain: fibronectin type III repeat homology <FN3F>

F:630-713/Domain: fibronectin type III repeat homology <FN3G>

F:721-810/Domain: fibronectin type III repeat homology <FN3H>

F:811-1187/Product: protein tyrosine phosphatase phi, long form #status predicted <PHL>

F:811-875, 876-1187/Product: protein tyrosine phosphatase phi, short form #status predicted <PHL>

F:819-843/Domain: transmembrane #status predicted <TM>

F:844-1187/Domain: intracellular #status predicted <INT>

F:901-1187/Product: protein tyrosine phosphatase phi, cytosolic form #status predicted <C>

F:1315-1155/Domain: protein-tyrosine-phosphatase homology <PTP>

F:75, 154, 189, 201, 227, 277, 286, 323, 359, 460, 489, 699, 711, 732, 789/Binding site: carbohydrate F:1107/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:1113/Binding site: substrate phosphate (Arg) #status predicted

Query Match 12.0%; Score 842; DB 1; Length 1187;

Best Local Similarity 24.4%; Pred. No. 4, 8e-39;

Matches 331; Conservative 203; Mismatches 436; Indels 389; Gaps 55;

Db 134 NVILTWKSNDRRAAEYKVKV-----HKENKKTIVHQP---MCNITGLRPAISYV 183

Db 39 SIIVSLASDVISPAASYVVKITGSKNVEFEFEFNSTLPPPIFRANHGL---YYI 94

Db 184 FSIIPGIGNETGDPRAVIVKITEPIVPSDLK-----ALGVKKAALSWNGGTASCR 237

Db 95 ITLVVAGNKNVTKRSRSRTVLTIKLPLPTYSVSIYYKKSPEGV----- 137

Db 238 VLLESIGSHEELTODSRQLQVNIIDK-----PGVQYININPYILO 276

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138 --LEIHYPEKXNVFTYVNISYEMGKAFRTMLYDFFPKKTVFPHMLPGICISYITQVL 195
139
277 SNKT--KODPLTEGGGLDASNTERSRAGSPAPVHDESLVGPVDPSSGQOSRDTVELLVG 334
196 SEATFNKSTLVEYSG--VSHPEKQHRATAPYP-----RNTSVRIVN 234
335 LEBGTRINATVYISQAANGTEGQ-----POLIERTNALIQUVDYAVANISATSL 382
235 LN-----KNWBEQSGSPFESEFMRSPETIE---KDRIF----- 265
383 TLIKWSDNESSNYTKIHVAGTSDSNLNVSPRAVILPGLRSTFYNTVCPVLADIE 442
266 -----HTEETPEPSGNIS-----S 280
443 GTPGFLQVHTPEVPSDFRVYVNVSTTEIGLAWMSHDA-----ESFOMHIIOEGAGNSRVE 497
281 GWP-----DPNSSDYETTSQPYWMDASATPSESDBEFVGLPMEYENNTWLS 327
498 ITTNQSIIGGLFPGTYKCEIYVKPGNGTEGASRTVCNRTVPSAVDIHVYVYTTBWM 557
328 EAEKPTAPAFSPFFVQOMILSWLPKPKPTAPADG-----PHIH---IERBENF 370
558 LDMKSPD-GASEVYVYHVLVBESK-----GSNHTSYDKAITLOGLPGT---LYN 603
371 TEYSTVBEAEHFAELKEPKKYTLVATTSASGSCETRESQAKSLSPISPTGEMIEE 430
604 ITISPEVDHVGDNSTAQYTRPSPNVNIDVSTTATATLSW-----ONFDDASPTYSYCL 659
431 LTERQ--HV-----SYHLSTT--ALMSWTSQENYNSTIVSV--VSL 469
660 LIEKAGNNSN-ATQVNTDIGITDATVTELLIPGSSYVEIFAQVBDGKLSLEPKKSFCTD 718
470 TCQOKESQRLERKQCYCTQVWNSKRIENLVPGAQYQVVMYLRKGPLI-----GPPS--D 521
719 PAMASF-----DEVVPKBP-ALVLMKCP-PEANNGFELEVSAGMANNATHLESCESE 771
522 PVTALVPTGIKIDMLPYLGPFAVLVSWTRKYLDVFRKYVEMF--YFNPAF---MTSE 575
772 NGTEYREVTYLNFTS-----YNISITVBSGKMAAFTRTYCTTG---ITDP 816
576 WTYTYELIAT-VSLTASVRIANLLPAMYNYNRYMTVMGD---PELSCCOSTISFIAP 631
817 PPDGSPNITSVSHNSYKVS-----GFEASHGPIKAYAVI-----LTT 856
632 V---APEITSEVEYFNLSLTYISWTYGDYDITDLSHRMLHMVYVAEGKKIKKSYTRVNMVT 687
857 GEAGHPADVLKATYYDDPKKGASTTYTYLIRTB-----EKGR 894
688 AILSLPREDIYNLSTACTGERSNTSLMRVLKLEPAPKSLFAVNKTQTSVTLIMVEBGV 747
895 S-----QSLSEVLYKEIIVGNBESTLYGYNGKLEPLGSRACVAGFTNITHPQ 943
748 ADFEVEFCQOVGSGLETKLQEPVAVSSHVVTI---SSLPATYNGSVTSFSH----- 797
944 NKGILDAESVYSPRSYDAVSLPQDPGVICAGVFGCIPGALVIVTVYVGGFIEMRK--- 999
798 -----DPSVPTFLIAVSTMVT-EMNPNVYVIVSLIISTLLIGLLVTLIIIRKQLM 850
1000 -RKDAKNNVESFSQIKP-----KKSLT---IRVENEAIFYKQOQADNSNGFA 1042
851 AREGAGCTFVNFALIERBDGKLRYNMSKNGLKRRKLTLPVQJLDDDAIYIKMAKOSDYKFS 910
1043 EYSEBDLKVGISOKYAAELAENNGKRRYNNVLLPYDISRYK-TLSVQHTSDYDYNANAYM 1101
911 LQFEBELKILGIDITHFAADPLANKCKRNTYILPYDSSRKVLLSMNEBEGADYINANYIIP 970
1102 GYHSKQFIATQGPLPNTLKDPMRWMEKXVAYAILMLTKCYEGORITXCEEYWP-SKOAQD 1160
971 GYNSPFGFIATQGPLPBTBDFWGMVVLQXSQOMIWMLTQCNBKKRKYVCDHMYPTBEP 1030
1161 YGDTIVAMTSIYVPEWTIRDPYTKAIIQTSNSHLRQPHFTSWDHDVY--DTTDLILNF 1218

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Db 1031 YGDITVEMTISEEDODMHRFRIN--YADEMODVHFNVTAMPDGHVPTANAESILQF 1088
 QY 1219 RYLVRDMKOSPESPILVHCSAGVGRTEGFIADBLIYOIEMENVVDYGYDLMR 1278
 Db 1089 VHVNRQOATKS--KGMIIHCSAGVGRTEGFIADBLIYOHIRHEFVDILGLVSEKRSYR 1146
 QY 1279 PLAVOTEDQVFLNQCV--LDIVRSQKSKVDLIYQNTT 1315
 Db 1147 MSWQTEBOYFIHQCVQVLMKMKKQOFCISDVIYENVS 1185

RESULT 15

S60613
 Protein-tyrosine-phosphatase (EC 3.1.3.48) U2 precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S60613
 R/Seiima, H.; Sawabe, T.; Inazawa, J.; Tsuruo, T.
 Oncogene 10, 1731-1738, 1995
 A/Title: Cloning, expression and chromosomal localization of a novel gene for protein ty
 A/Reference number: S60613; MUID:95273089; PMID:7753550
 A/Accession: S60613
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1216 <SEI>
 A/Cross-References: UNIPROT:Q16827; EMBL:Z48541; NID:9963058; PIDN:CAA8425.1; PID:93630
 C/Superfamily: Protein-tyrosine-phosphatase, receptor type O; fibronectin type III repes
 C/Keyword: phosphoprotein, phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F/329-626/Domain: fibronectin type III repeat homology <3PR>
 F/962-1184/Domain: protein-tyrosine-phosphatase homology <PRP1>
 F/1136/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1142/Binding site: Substrate phosphate (Arg) #status predicted

Query Match 11.9%; Score 839; DB 2; Length 1216;
 Best Local Similarity 24.2%; Pred. No. 7.3e-39;
 Matches 333; Conservative 200; Mismatches 449; Indels 394; Gaps 57;

QY 134 NVILWKSNDTAASEKTYVK-----HKMENKTIIVVHQP--WCNITGLRPTSIV 183
 Db 39 NIVVLEASDVISPAVYVVKITGESKNVFEFESEFNSTLPPVIFKASYGL-----YYI 94
 QY 184 FSITGIGNETGDDPRVIVKITEPIVPSDLRVALGVGRKALMSWNGNGTASCRVLESI 243
 Db 95 ILLVNVGNVVTKPRSRITVTKPLPV----- 122
 QY 244 GSHEELTQDSRLQVNISDLKP---GYQYINIPYLLQSNKTGKGPLGTEGGLDASNTERS 299
 Db 123 -----SVSITVDYKPSPEETGVLFELH-YPEKTNVVFRRVNI SYWGGKDPRTM--- 166
 QY 300 RAGSPFAPVHDSLVGPVDPSSGQSRDETVLLVGLFEGTRYNATVYQAAANGTEGQPOA 359
 Db 167 -----LYKDFEFGK-----KTVFNHMLPGMCMCSNITPQLVCEATFNKSTV 205
 QY 360 IEF-----RTNAI--GVFDVAVNISATSLTLMKVSNDNESSNYTKIHVAGET 407
 Db 206 VEYSVSHHPKQHRAPRPQNISIRIVNLKNN---WE---EQSANFEESPMNSOD 257
 QY 408 DSSNLNVSEPRAVIFGLRSSTFFNYITVCPVLGDIETGPGFLQVHTPPVPS-----DF 460
 Db 258 T-----IKEKLFHPT-----EETPEIPSGNISSGWPDF 286
 QY 461 RTVVSTTEIGLAWGSHDA-----ESFQMHTQEGAGNSRVEITNQSIIIGLPGTKY 515
 Db 287 NSSDVEITTSQPYWWSASAPSEDEFPVSLPMEYENNSTLSETEKSTSGSFFFPVOMI 346
 QY 516 CFEIIVKGPNGTEGASRTVCNRVPSAVFDIHV-----VYVTTTMMMLDMKSPD 564
 Db 347 LTMLEPKRPTAFD-----FHIIHREENFTVYLMVDEBAHFVALEKRP- 391
 QY 565 GASEVYVHLVIESKRGSHHTSTYDKATLQGLIPGLLYNITISPEVDHWGDPNSTAQYT 624
 Db 392 --GKYKLSVTTFSSSGSCETRKSSAKSL-----SFYISPSGE--WIEELT---E 434

QY 625 RPSNVSNIDVSTNTAATLSW-----QNPDDASPTYSYCLLIERKAGNSN-ATQVVPDICI 679
 Db 435 KPOHVS-FHVLSTTI-ALMSWTSSQENNSTIVV-VSLTCQKQKESQRLKQYCTQVNS 491
 QY 680 TDAVTELLIPGSSYVEIFAOVGDGIXLEPGRKSFCTDPASMAF-----DCEVVKEP 734
 Db 492 SKPIIENLVPGAQVQVVIYLRKPLI-----GPPS---DPVTFALVPTGIDMLLYLGP 543
 QY 735 -ALYKATCP--PGANAGELEVSSGAMNATHLESCESENGTEVRYEYTLNISTS----- 788
 Db 544 TAVVLSTWTRPYLGVFRKVVEMF--YFNPAF---MTSEWTTYEIAAT-VSLTASVRIA 596
 QY 789 -----YNISITVSCGKMAAPTRNTCTTG-----ITDPPDQSPNITSVSHSVKVF 837
 Db 597 NLLPAMTYNFRVYVMTGDD--PELSCDSSITFTAPV---APEITSVETNSLIYI 649
 QY 838 S-----GFEASHQPIKAVAVILTTGBAGHSADVLKTYVDPEFKGAS----- 879
 Db 650 SWTYGDDTDTLDSHRMLHMMVV--TEGK-----KKIKSVTRVMTAIIISLPP 695
 QY 880 -DTVVTYLIRTEERGRQSLSEVLKYE-----IDVGNESTTLGYN----- 919
 Db 696 GDTYVLSVTCTCTERGSNTSMRLRVKLEPAPPKSLFANVKTQTSVTLMLVEGVADPEKVP 755
 QY 920 -----GKLEPLGSRACVAGFTNITFHPQKGLIDGAESEY 954
 Db 756 FQHGSSQKTKLQSPVAVSHVVTISSLRATVSCVTSFSH-----DSPSV 803
 QY 955 VSEBRYSDAVSLPDDPGVIGAVFGCIFGALVITVVGGFIFWRK----- 999
 Db 804 PTFIAVSTMTV-EMNPVNVVIVSLAILSTLIGLITVTLIIIRKHLQMARREGAGTFAN 862
 QY 1000 -----RKDAK-----NNEVSFSQIKP-----KSKL---IRVEN 1025
 Db 863 CASLERGKTPYCNCRSIFAFLLPILBSCMTDYPLAFYINPWSKNGIKRKLTPVQLDD 922
 QY 1026 FEAYFKQOADSNGCFAEYEDKLVGISQPKYAELAEENRGQRVNNVLPYDISRYKL- 1084
 Db 923 FDAYIKDMADSDYKFSLQFEELKTLGLDIPHPAADLPINRCORRTNIIIPYFSRVLY 982
 QY 1085 SVQTHSTDDYINANNMNGSHSKDFTATGQPLPNTLKDFRRMYEKQNVYAIIMLTICVQD 1144
 Db 983 SNEEBEGADYINANNYPGVNSPOEYIATOGPLPETRNDPEKVVLOQKSOIYVWLTOCNEK 1042
 QY 1145 GRTCEBYNP-SKQAOYDGDITVAMTSEIVLPMTIRDFTVKNIIQTSSESHPLQFPTSM 1203
 Db 1043 RRYKCHYWFTEEPRIAYGDIYEMISEEDODMACHRIN--YADEMODVHFNVTAM 1100
 QY 1204 PDHGVF--DTTDLINFRYIVRDYMKOSPESPILVHCSAGVGRTEGFIADBLIYOIEN 1261
 Db 1101 PDHGVPTANAASIILOFVHVNRQOATKS--KGMIIHCSAGVGRTEGFIADBLIYOHIR 1158
 QY 1262 ENTVDYVGYIYDLMRRLPVQTEDOYVFLNQCV--LDIVRSQKSKVDLIYQNTT 1315
 Db 1159 HEFVDIILGLVSEKRSYRMSWQTEBOYFIHQCVQVLMKMKKQOFCISDVIYENVS 1214

Search completed: May 10, 2005, 19:05:40
 Job time : 69 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:46:26 ; Search time 203 Seconds
(without alignments)
3372.659 Million cell updates/sec

Title: US-09-516-728A-4
Perfect score: 7030
Sequence: 1 MKPAPARARLPPRSFGRLWA.....TIYENLAPVTFKNGYIA 1337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7023	99.9	1337	1	PTPJ_HUMAN
2	4510.5	64.2	1238	1	Q8K3Q2 mus musculus
3	4508.5	64.1	1238	1	PTPJ_MOUSE
4	4499.5	64.0	1216	2	Q62864 ratu
5	4483.5	63.8	1238	2	Q8C1W9 mus musculus
6	2784	39.6	539	2	Q6P4H4 homo sapien
7	2752.5	39.2	1406	2	Q9W6V5 gallus galli
8	2184	31.1	425	2	Q9NPR5 homo sapien
9	1847	26.3	361	2	Q61373 mus musculus
10	1259.5	17.9	1998	2	Q8C1W2 mus musculus
11	1242	17.7	1997	1	PTPJ_HUMAN
12	1239	17.6	1956	1	Q6M2F6 homo sapien
13	1219.5	17.3	1102	2	Q80VW7 mus musculus
14	1176.5	16.7	1115	2	Q8HDA3 homo sapien
15	1130	16.1	1118	2	Q15426 homo sapien
16	1046.5	14.9	1631	2	Q86NM9 drosophila
17	1043.5	14.8	1556	2	Q81R87 drosophila
18	1043.5	14.8	1631	1	PTPJ_DROME
19	1043.5	14.8	1962	2	Q9VYU1 drosophila
20	993.5	14.1	579	2	Q9J107 mus musculus
21	991.5	14.1	1705	2	Q9ERK5 mus musculus
22	990.5	14.1	1705	1	PTPJ_MOUSE
23	969	13.8	1767	2	Q9W4F5 drosophila
24	964	13.7	1607	2	Q81R50 drosophila
25	956	13.6	1711	1	PTPJ_RAT
26	955	13.6	1767	2	Q24495 ratu
27	922	13.1	1064	2	Q8SXB2 drosophila
28	906	12.9	958	2	Q8B1W7 m mus muscu
29	879	12.5	1912	1	PTPJ_HUMAN
30	864	12.3	2302	2	Q88488 ratu
31	853.5	12.1	1198	2	Q9J1U0 mus musculus

32	852	12.1	1267	2	Q98945 gallus galli
33	849.5	12.1	1216	2	Q62797 ratu
34	846	12.0	1896	2	Q91AJ1 xenopus lae
35	842	12.0	1187	2	Q28613 oryctolagus
36	841	12.0	1226	2	Q7TSY7 mus musculus
37	839	11.9	1216	1	PTPJ_HUMAN
38	834.5	11.9	1226	2	Q9ERN5 mus musculus
39	826	11.7	1894	2	Q64487 mus musculus
40	822.5	11.7	1788	2	Q91AJ0 xenopus lae
41	817	11.6	1367	2	Q20120 caenorhabdi
42	808.5	11.5	1887	2	Q9QK67 ratu
43	807	11.5	1898	2	Q64604 r protein-t
44	806.5	11.5	1898	2	Q9EQ17 mus musculus
45	804	11.4	1948	1	PTNS_HUMAN

ALIGNMENTS

RESULT 1
PTPJ_HUMAN STANDARD; PRT; 1337 AA.
ID Q12913; Q15255; Q8NHM2;
AC Q12913; Q15255; Q8NHM2;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTP eta) (Protein-tyrosine phosphatase receptor type J) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen).
GN Name=PTPJ; Synonyms=DEP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=95024024; PubMed=7937872;
RX Oestman A., Yang O., Tonke N.K.;
RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density."
RT Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
RN [2]
RP PRO-276
RC TISSUE=Colon;
RX MEDLINE=22084388; PubMed=12089527; DOI=10.1038/ng903;
RX Ruivenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vlieck C.,
RA Csikos T., Kloue A.M., Tripodi S., Petrakis A., Boerlinter L.,
RA Groot P.C., Lindeman J., Mooi W.J., Meijer G.A., Scholten G.,
RA Dauterive H., Paces V., van Zandwijk N., van Ommen G.J.B., Demant P.;
RT "Ptpj is a candidate for the mouse colon-cancer susceptibility locus Sccl and is frequently deleted in human cancers."
RL Nat. Genet. 31:295-300(2002).
CC -1- FUNCTION: May contribute to the mechanism of contact inhibition of cell growth.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- and O-glycosylated.
CC -1- DISEASE: Defects in PTPJ are found in cancers of colon, lung, and breast.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -1- SIMILARITY: Contains 3 subfamily.
CC -1- SIMILARITY: Contains 9 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -1- DATABASE: NAME=PROJ; NOTE=CD guide CD148 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/row/cd/cdi48.htm".

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL, U10886; AAB36687.1; -

DR EMBL, D37781; BAA07035.1; -

DR EMBL, AF387844; AAM69432.1; -

DR EMBL, AF387823; AAM69432.1; JOINED.

DR EMBL, AF387824; AAM69432.1; JOINED.

DR EMBL, AF387825; AAM69432.1; JOINED.

DR EMBL, AF387826; AAM69432.1; JOINED.

DR EMBL, AF387827; AAM69432.1; JOINED.

DR EMBL, AF387828; AAM69432.1; JOINED.

DR EMBL, AF387829; AAM69432.1; JOINED.

DR EMBL, AF387830; AAM69432.1; JOINED.

DR EMBL, AF387831; AAM69432.1; JOINED.

DR EMBL, AF387832; AAM69432.1; JOINED.

DR EMBL, AF387833; AAM69432.1; JOINED.

DR EMBL, AF387834; AAM69432.1; JOINED.

DR EMBL, AF387835; AAM69432.1; JOINED.

DR EMBL, AF387836; AAM69432.1; JOINED.

DR EMBL, AF387837; AAM69432.1; JOINED.

DR EMBL, AF387838; AAM69432.1; JOINED.

DR EMBL, AF387839; AAM69432.1; JOINED.

DR EMBL, AF387840; AAM69432.1; JOINED.

DR EMBL, AF387841; AAM69432.1; JOINED.

DR EMBL, AF387842; AAM69432.1; JOINED.

DR EMBL, AF387843; AAM69432.1; JOINED.

DR HSR, 138670; 138670.

DR PIR, P18052; 18052.

DR Gene, HGNC:3673; PTPRJ.

DR MIM, 600925; -

DR GO, GO:0005887; C:integral to plasma membrane; TAS.

DR GO, GO:0005001; F:citronemembrane receptor protein tyrosine pho. . .; TAS.

DR GO, GO:0007267; P:cell-cell signaling; TAS.

DR GO, GO:0006470; P:protein amino acid dephosphorylation; TAS.

DR GO, GO:0007163; P:transmembrane receptor protein tyrosine kin. . .; TAS.

DR InterPro, IPR003961; FN_III.

DR InterPro, IPR008957; FN_III-like.

DR InterPro, IPR000387; TYR phosphatase.

DR InterPro, IPR000242; TYR_PP.

DR Pfam, PF00041; fn3; 6.

DR Pfam, PF0102; Y_phosphatase; 1.

DR PRINTS, PR00700; PRTPHPTASE.

DR SMART, SMO0060; FN3; 8.

DR SMART, SMO0194; PTPC; 1.

DR PROSITE, PS00853; FN3; 9.

DR PROSITE, PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE, PS00056; TYR_PHOSPHATASE_2; 1.

DR PROSITE, PS00055; TYR_PHOSPHATASE_PTP; 1.

DR Disease mutation; Glycocyproline; Hydrolase; Protein phosphatase;

KW Repeat; Signal; Transmembrane.

FT SIGNAL 1 35 Potential.

FT CHAIN 36 1337 Protein-tyrosine phosphatase etc.

FT DOMAIN 36 975 Extracellular (Potential).

FT TRANSMEM 976 996 Potential.

FT DOMAIN 997 1337 Cytoplasmic (Potential).

FT DOMAIN 119 205 Fibronectin type-III 1.

FT DOMAIN 207 291 Fibronectin type-III 2.

FT DOMAIN 271 364 Fibronectin type-III 3.

FT DOMAIN 365 452 Fibronectin type-III 4.

FT DOMAIN 453 538 Fibronectin type-III 5.

FT DOMAIN 540 620 Fibronectin type-III 6.

FT DOMAIN 622 717 Fibronectin type-III 7.

FT DOMAIN 720 811 Fibronectin type-III 8.

FT DOMAIN 816 902 Fibronectin type-III 9.

FT DOMAIN 1065 1337 Protein-tyrosine phosphatase.

FT	ACT_SITE	1239	1239	Phosphocysteine intermediate (By similarity).
FT	CARBOHYD	72	72	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	82	82	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	93	93	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	104	104	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	142	142	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	172	172	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	192	192	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	231	231	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	258	258	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	278	278	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	342	342	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	351	351	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	376	376	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	391	391	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	396	396	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	413	413	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	431	431	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	501	501	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	525	525	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	536	536	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	582	582	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	603	603	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	618	618	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	628	628	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	637	637	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	666	666	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	669	669	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	761	761	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	772	772	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	784	784	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	790	790	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	824	824	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	910	910	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	937	937	N-linked (GlcNAc. . .) (Potential).
FT	VARIANT	214	214	R -> C (in colon cancer; somatic mutation).
FT	VARIANT	276	276	/FTID=VAR_015905.
FT	VARIANT	276	276	Q -> P (in colon cancer; somatic mutation; dbSNP:1566734).
FT	CONFLICT	261	261	/FTID=VAR_015906.
FT	CONFLICT	918	929	G -> D (in Ref. 1).
FT	SEQUENCE	1337 AA; 145926 MW; E6752D521C4B6AFE CRC64;		YNGKLEPLGSGYR -> LQWAGTSGLLP (in Ref. 2).
Query Match	99.9%; Score 7023; DB 1; Length 1337;			
Best Local Similarity	99.9%; Pred. No. 0;			
Matches 1336; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 MKPAREARLPSPSPGLRMLPLLLLRGLGQILGAGTSPSPIDPSVATVANGENGITQ	60		
DB	1 MKPAREARLPSPSPGLRMLPLLLLRGLGQILGAGTSPSPIDPSVATVANGENGITQ	60		
QY	61 ISSTASFKHONGTGPVEVTNTSEDESSGANDSLRTPGSGNGTGDASQKTPSSSTGPS	120		
DB	61 ISSTASFKHONGTGPVEVTNTSEDESSGANDSLRTPGSGNGTGDASQKTPSSSTGPS	120		
QY	121 PVEDIDAVSISPNVLLTKSNDTASFKYVVKHMEKETTIVHGWNCINTGIRPAT	180		
DB	121 PVEDIDAVSISPNVLLTKSNDTASFKYVVKHMEKETTIVHGWNCINTGIRPAT	180		
QY	181 SYVFTIPGIGNETWDPRIKIVTEPIVSDLRVALTGVRKAALSMNGNGTASGRVLL	240		
DB	181 SYVFTIPGIGNETWDPRIKIVTEPIVSDLRVALTGVRKAALSMNGNGTASGRVLL	240		
QY	241 ESIGSHBELTQDSRLQVNIIDLPKGVQVINIPYLLQSNKTKDPLGTGGLDASNTGSR	300		
DB	241 ESIGSHBELTQDSRLQVNIIDLPKGVQVINIPYLLQSNKTKDPLGTGGLDASNTGSR	300		
QY	301 AGSPPTAPVHDESLVGVVDSSGQGSQSDTGVLLVGLFGRNRYNATYYSQANANGTEGPQAI	360		
DB	301 AGSPPTAPVHDESLVGVVDSSGQGSQSDTGVLLVGLFGRNRYNATYYSQANANGTEGPQAI	360		

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QY 361 EFRFNAIOVPDYTAVNISATSLTLMKYSNDNESSNTYKIHVAGETDSSNLNVSEPAV 420
DB 361 EFRFNAIOVPDYTAVNISATSLTLMKYSNDNESSNTYKIHVAGETDSSNLNVSEPAV 420
QY 421 I PGLRSSFTFYNTITVCPVLGDI EGTGFLQVHTPPVPSDFRVTVSTTEIGLAWSSDAE 480
DB 421 I PGLRSSFTFYNTITVCPVLGDI EGTGFLQVHTPPVPSDFRVTVSTTEIGLAWSSDAE 480
QY 481 SFOHMTTQEGAGNSRVEITTNOSIIIGLFPCTKCFEIVPGRNGTGASTVONRTP 540
DB 481 SFOHMTTQEGAGNSRVEITTNOSIIIGLFPCTKCFEIVPGRNGTGASTVONRTP 540
QY 541 SAVFDIHVVYTTTMMMLDMKSPDGA SEVYHLVESHKSHSTYTKAITLOGLIGT 600
DB 541 SAVFDIHVVYTTTMMMLDMKSPDGA SEVYHLVESHKSHSTYTKAITLOGLIGT 600
QY 601 LYNITISPEVDHWDPNSTAQTTPSPSVNSIDVSTNTTAATLSMNFDDASPTVSYCL 660
DB 601 LYNITISPEVDHWDPNSTAQTTPSPSVNSIDVSTNTTAATLSMNFDDASPTVSYCL 660
QY 661 IEKAGNSSNATQVTDIGITDATTVELIPGSSYTYEIRAQVDDGKSLDEPKKSCCTPA 720
DB 661 IEKAGNSSNATQVTDIGITDATTVELIPGSSYTYEIRAQVDDGKSLDEPKKSCCTPA 720
QY 721 SMASPDCEVPEPALVLMKTCPPGANAGFELEVS SGAMNATHLESCSENGTEYREV 780
DB 721 SMASPDCEVPEPALVLMKTCPPGANAGFELEVS SGAMNATHLESCSENGTEYREV 780
QY 781 TYLNFSTSYNISITTVSCGKMAAPTRNTCTTGITDPPPDGSPNITSVSHSVKXFGSG 840
DB 781 TYLNFSTSYNISITTVSCGKMAAPTRNTCTTGITDPPPDGSPNITSVSHSVKXFGSG 840
QY 841 EASHGPICAKYAVIITLTERAGHPSADV LKTTYDPFKKASDITYVTLIRTEEGRSQSLSE 900
DB 841 EASHGPICAKYAVIITLTERAGHPSADV LKTTYDPFKKASDITYVTLIRTEEGRSQSLSE 900
QY 901 VLKKEIDVGNESSTLTGYNGKLEPLGSRACVAGFNTTFPHQNGLIDGAEYSFSPRY 960
DB 901 VLKKEIDVGNESSTLTGYNGKLEPLGSRACVAGFNTTFPHQNGLIDGAEYSFSPRY 960
QY 961 SDAVSLPODPGVICGAVFGCIFGALVITYVGGFIFMRKKRKDKADKONNEVSFSQIKPKSKL 1020
DB 961 SDAVSLPODPGVICGAVFGCIFGALVITYVGGFIFMRKKRKDKADKONNEVSFSQIKPKSKL 1020
QY 1021 IRVENFEAYFKKQADSNCGFAEYEDLKLVGISQPKTAAELAEENRGKRRYNNVLPYDIS 1080
DB 1021 IRVENFEAYFKKQADSNCGFAEYEDLKLVGISQPKTAAELAEENRGKRRYNNVLPYDIS 1080
QY 1081 RVKLSVOTHSTDDYINANMPPGHSKODFIATOGFLPNTLKDPMRWMEKNNYATIMLTK 1140
DB 1081 RVKLSVOTHSTDDYINANMPPGHSKODFIATOGFLPNTLKDPMRWMEKNNYATIMLTK 1140
QY 1141 CVEQRTCEBYEWPBKQADYDITVAMTSEIVLPEMTIRDTFTVKNIOSESHPROHF 1200
DB 1141 CVEQRTCEBYEWPBKQADYDITVAMTSEIVLPEMTIRDTFTVKNIOSESHPROHF 1200
QY 1201 TSMWPHGVBDTDLINFRYLVADYMKOSPSPSPILVHCSAGVGTGTFIALDRLIYOIE 1260
DB 1201 TSMWPHGVBDTDLINFRYLVADYMKOSPSPSPILVHCSAGVGTGTFIALDRLIYOIE 1260
QY 1261 NENTVDVYGIYVDLAMHRLPMQOTEDQVYFLNOCVLDIRSOKDKRULIYONTAMTY 1320
DB 1261 NENTVDVYGIYVDLAMHRLPMQOTEDQVYFLNOCVLDIRSOKDKRULIYONTAMTY 1320
QY 1321 ENLAPVTTEGKNGYIA 1337
DB 1321 ENLAPVTTEGKNGYIA 1337
RESULT 2
Q8K3Q2 PRELIMINARY; PRT; 1238 AA.
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AC Q8K3Q2,
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE PTPRJ.
GN Name=Pcpj;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ST5;
RA van Wezel T., Ruijvenkamp C.A.L., Zanon C., Stassen A.P.M., Vlcek C.,
RA Csikos T., Tripodi N., Groot P.C., Dauverse H., van Ommen G.J.B.,
RA Demant P.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039232; AAK98640.1; -.
DR HSSP; P18052; 1YPO.
DR MGD; MGI:104574; Pcpj.
DR GO; GO:0005615; C:intracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0007507; P:heart development; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SMO0060; FN3; 7.
DR SMART; SMO0194; PTPc; 1.
DR PROSITE; PS00853; FN3; 5.
DR PROSITE; PS00883; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydroxylase.
SQ SEQUENCE 1238 AA; 136772 MW; 0D02F5EF8E23C0B2 CRC64;

Query Match 64.2%; Score 4510.5; DB 2; Length 1238;
Best Local Similarity 67.2%; Pred. No. 3.6e-247;
Matches 901; Conservative 108; Mismatches 226; Indels 105; Gaps 12;

QY 1 MKPAREARLPBRPGRLMALPLLLRLQLIICAGTSPRPDPVAVATGENGITQ 60
DB 1 MKPAREARLPBRPGRLMALPLLLRLQLIICAGTSPRPDPVAVATGENGITQ 60
QY 61 ISSTAEPHKONGTGPQVETNTSEDSGSGANDSLRTPGSGNGTDGASQKTPSSTPS 120
DB 61 ISSTAEPHKONGTGPQVETNTSEDSGSGANDSLRTPGSGNGTDGASQKTPSSTPS 120
QY 44 ----- 43
DB 44 ----- 43
QY 121 PVFDIKAVISPTNVILTWKSNDRASRYKYVVKHKEKNTIYVHQPKCNITGLRPAT 180
DB 121 PVFDIKAVISPTNVILTWKSNDRASRYKYVVKHKEKNTIYVHQPKCNITGLRPAT 180
QY 44 --FDIEAV-VAPTSVILTWKNDGASACR--IKKESNLTFPVKQNTSCNITGLSPGT 98
DB 44 --FDIEAV-VAPTSVILTWKNDGASACR--IKKESNLTFPVKQNTSCNITGLSPGT 98
QY 181 SYVPSITGIGNETMGDPDRVAKVITEPIVSDLDVALTGKAKALMSWNGGTASCRVL 240
DB 181 SYVPSITGIGNETMGDPDRVAKVITEPIVSDLDVALTGKAKALMSWNGGTASCRVL 240
QY 99 SYTFSIISVTNETLNK---TITTEPVPVSDLHVTSGVIAQARLTWNNAGTASVRLIT 154
DB 99 SYTFSIISVTNETLNK---TITTEPVPVSDLHVTSGVIAQARLTWNNAGTASVRLIT 154
QY 241 ESIGSHEELTQDSRLQVNIIDLKPGVQYINIPYLL-QSNKTKCPDLATEGGLDASNTERS 299
DB 241 ESIGSHEELTQDSRLQVNIIDLKPGVQYINIPYLL-QSNKTKCPDLATEGGLDASNTERS 299
QY 155 EELTHS-----SVNISGLKGTN---NTFAPEPSENEQADFAVAEVPDANGTKRI 203
DB 155 EELTHS-----SVNISGLKGTN---NTFAPEPSENEQADFAVAEVPDANGTKRI 203
QY 300 RAGSPTAFVHDESLVGPVDPSSGQSDRTVELVLGLEBGTRYNATVYSQAANGTEGQPA 359
DB 300 RAGSPTAFVHDESLVGPVDPSSGQSDRTVELVLGLEBGTRYNATVYSQAANGTEGQPA 359
QY 204 PVTNLSQP-HKNSLAS-VDPSPGQDPSLTETILLTDLKEDTQYNATVYSQAANGTEGQPRN 261
DB 204 PVTNLSQP-HKNSLAS-VDPSPGQDPSLTETILLTDLKEDTQYNATVYSQAANGTEGQPRN 261
QY 360 IEFRTNAIOVPDYTAVNISATSLTLMKYSNDNESSNTYKIHVAGETDSSNLNVSEPA 419
DB 360 IEFRTNAIOVPDYTAVNISATSLTLMKYSNDNESSNTYKIHVAGETDSSNLNVSEPA 419
QY 262 KVFKNSTQVSDVPRAMNISASSMTLTWKSNDGSTRISIVYKIHVAGGTHSVNQVYKTEA 321
DB 262 KVFKNSTQVSDVPRAMNISASSMTLTWKSNDGSTRISIVYKIHVAGGTHSVNQVYKTEA 321
QY 420 VIPGLRSSFTFYNTITVCPVLGDI EGTGFLQVHTPPVPSDFRVTVSTTEIGLAWSSDA 479
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Db      322  IILGLSSSTLYNITVHFLGOTEGTPEGLQVYVTSPPQVSPFRNTVNSTALIGLAMSNDNS 381
Qy      480  ESQOMHTTOGAGNSRREITNNSIIIGLFPGTKICEFELVPGNGTGCASRTVCNRTV 539
Db      382  KSFEIFKQDGEKHNRASTGNSYMEDLKPGTSYHFEIIPRGPDTGSLSTVNGSYTD 441
Qy      540  PSAVFDIHVVYVTTTEWMLDMKSPDGAEEVYHLVYESKHGS-NHSTYDKAITLQGLP 598
Db      442  PSAVTDIRVNITSTTEQLEMONTDASGTYHLVLESAGSILRTNSSOKMTTIGSLTP 501
Qy      599  GILYNTITISPEVDHWGDPNSTAQYTRPSNVSNIDVSTNTAATLSWONFDDASPTYSYC 658
Db      502  GILYNTITISPEVDHWGDPNSTAQYTRPSNVSNIDVSTNTAATLSWONFDDASPTYSYC 561
Qy      659  LLEKAGNSNAQVNT-DIGITDAVTELIPSSSTVTEIFAOVGIGISLEPRGRSFCT 717
Db      562  VLLKKTGDSNVTSNFTKDPST--LIPELIPGVASTYVILQVGDGTTSLPQWMLFCT 618
Qy      718  DPASMASPDEEVVPEKPEPALVAKWTCPPGANAGPELEVSQAMNNAATHLSSCSSENGTEYR 777
Db      619  EPESTVTSFHEEVPEKPEPALVAKWTCPPGANAGPELEVSQAMNNAATHLSSCSSENGTEYR 678
Qy      778  TEVTYINFTSTYVNIISTVYSCGMAAPRTNTCTTGTIDPPPDGSPNITSVSHNSVYKVF 837
Db      679  TEVAYINFTSTYVNIISTVYSCGMAAPRTNTCTTGTIDPPPDGSPNITSVSHNSVYKVF 738
Qy      838  SGFEASHGPIKAYAVILTTGEAGHPSADVLKTYDQDFKAGADTYVYILRIEHEGRGQS 897
Db      739  SGFEASHGPIKAYAVILTTGEAGHPSADVLKTYDQDFKAGADTYVYILRIEHEGRGQS 798
Qy      898  LSEVLKYEIDVGNESSTLLGYNGKLEPLGSYRACVAGFTNITFPHQNKGLIDGASYSYF 957
Db      799  LSEVLKYEIDVGNESSTLLGYNGKLEPLGSYRACVAGFTNITFPHQNKGLIDGASYSYF 858
Qy      958  SHYSDVSLPDPBGVTCGAVFGICRGALVYIVVGGFIFMRKKRKAANNESVFSQIKRKC 1017
Db      859  SHYSDVSLPDPBGVTCGAVFGICRGALVYIVVGGFIFMRKKRKAANNESVFSQIKRKC 918
Qy      1018  SKLIRVENFEAYFKKQADNSNGFAEEYEDLKLVLGISOPKVAELAEKNGKRYNNVLPY 1077
Db      919  SKLIRVENFEAYFKKQADNSNGFAEEYEDLKLVLGISOPKVAELAEKNGKRYNNVLPY 978
Qy      1078  DISRYKLASVQTHSTDDYINANMPGYSKKDFIATQGPLLTKDFPMMWEKKNYALIM 1137
Db      979  DISRYKLASVQTHSTDDYINANMPGYSKKDFIATQGPLLTKDFPMMWEKKNYALIM 1038
Qy      1138  LFKCYEGRTKCEEYWPSSKQADYGDITVAMTSEIVLEPWTTRDFTYKNIQTSSEHPIRQ 1197
Db      1039  LFKCYEGRTKCEEYWPSSKQADYGDITVAMTSEIVLEPWTTRDFTYKNIQTSSEHPIRQ 1098
Qy      1198  FHFSTMPDHGVPDITDLINFRYLVADYWKQSPSPSPILVHCSAGVGTGTFIADRLIY 1257
Db      1099  FHFSTMPDHGVPDITDLINFRYLVADYWKQSPSPSPILVHCSAGVGTGTFIADRLIY 1158
Qy      1258  QLENENTYDVYGIYVDLAKMRPLMQTEBQVYFLNQCVLDIVRSQKSDKVDLIYQNTTAM 1317
Db      1159  QLENENTYDVYGIYVDLAKMRPLMQTEBQVYFLNQCVLDIVRSQKSDKVDLIYQNTTAM 1218
Qy      1318  TIYENLAPVTPFGKNGYIA 1337
Db      1219  TIYENLAPVTPFGKNGYIA 1238

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RESULT 3
PTPJ_MOUSE STANDARD: PRT: 1238 AA.
AC 064455:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTP beta-like tyrosine phosphatase) (Protein-tyrosine phosphatase)

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DE Receptor type J (Susceptibility to colon cancer-1).
GN Name=ReprJ; Synonyms=ByP, Sccl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MRL-LPR/LPR;
RX MEDLINE=96140699; PubMed=8549806; DOI=10.1016/0014-5793(95)01415-2;
RA Kuremochi S., Matsuda S., Matsuda Y., Saitoh T., Ohnogi M.,
RA Yamamoto T.;
RT "Molecular cloning and characterization of ByP, a murine receptor-type
RT tyrosine phosphatase similar to human DEP-1.";
RL FBSB Lett. 378:7-14(1996).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in every tissue examined.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 3 subfamily.
CC -1- SIMILARITY: Contains 8 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D45212; BA00146.1; -.
DR PIR: S68700; S68700.
DR HSSP: P18052; IYFO.
DR MGD: MGI:104574; PcpJ.
DR GO: GO:0007507; P:heart development; IMP.
DR GO: GO:0001570; P:vasculogenesis; IMP.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000387; Tyr_PP.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; fn3; 6.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PRTYPHPTAS.
DR SMART: SM00060; FN3; 7.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS50853; FN3; 7.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Glycoprotein; Hydrolase; Protein phosphatase; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 28
FT CHAIN 29 1238
FT DOMAIN 29 876
FT TRANSHEM 897
FT DOMAIN 898 1238
FT DOMAIN 170 1230
FT DOMAIN 267 354
FT DOMAIN 356 440
FT DOMAIN 442 527
FT DOMAIN 529 618
FT DOMAIN 620 712
FT DOMAIN 717 803
FT DOMAIN 966 1238
FT ACT_SITE 1140 1140
FT CARBOHYD 62 62
FT CARBOHYD 78 78
FT CARBOHYD 85 85
FT CARBOHYD 90 90

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Db	382	KSPIFIKODGEKHNASNGOSVYMEDLKPGTSYHFEIIPRPGDGTGELSGSTVN	444
Oy	540	PSANFDHVVYVTTTMMWMDMKSPDGASEVYHVIKSKGS-NHSTYDAITLQGLIP	598
Db	442	PSAATDIRVANIITTEMOLEQNTDDASGYTHLVKESKGSIIRTSSQKMTIVGSLTP	501
Oy	599	GTLYNITISPEVDHVMGDPNSTAQYTPRSVNSINDVSTNTAATLSQNFDDASPTYSC	658
Db	502	GTLYNITIFPEVDIOGISMNSIQTTPRSSVSHLEVNTTTTALIRKMDPAASAVAS	561
Oy	659	LIIKAGNSSNAIQVVT-DIGITDAVTELIPOSSSYTVEIIPAQVGDGKSLIEPKRKECT	717
Db	562	VLIKTDGDSNVTSNFKPDPSI---LIPELIPGVSYTYKILTOVGDDGTTSVLPKMNIFCT	618
Oy	718	DPAMASFDCEVNVKEKBPALVLYKMTCPGCAANAGEFLEYSSGAMNNAITLESSESSNGEYR	777
Db	619	EPEVTSFHCCVNVKEKBPALVLYKMACPGMVTGTFELGVRSDSDWMDMTLENTSDDTBECR	678
Oy	778	TEVYLVFSTSYNISITVSSCGKMAAPTRNTCTGTIDPDPDGSPIVTSVSHSVYKF	837
Db	679	TEVAYLNFSTSYNISITATLSGKMAAPLQNICTGTIDPDPDGSPIVTSVSHSVYKF	738
Oy	838	SGFEASHQPIKAVAVIITTEBAGHPASADVLYKYTDFPKGASDTYVYLLIFTEKGSQS	897
Db	739	SGFEASHGPIKAVAVIITTEGAAQPSADVLYKYTJEDPKRGASDPTVYVYLLIRIEKGSQSG	798
Oy	898	LSEVLKAEIDVGNSTLGYNGKLEJPELGSYRAVCAFPNTTTFHPKGLIDGAGESYSF	957
Db	799	LSEVLANEIDVGNOSTLGYNGKLEJPELGSYRAVCAFPNTTNYLQNDGLNGESYSVF	858
Oy	958	SRYSDAVSLPDDPVIICGAVFGCIFGALVVTYVGGCIFWKRKRKXDAKNNEVSFSQIKPK	1017
Db	859	SPYSEANFLPDDPVIICGAVFGCIFGALVITAVGGCIFWKRKRKXDAKNNEVSFSQIKPK	918


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Db 595 CMEBAQVDSLHCCEVVPKPEPALVILKMACPCPGNWSGFEIGVRSDADAMNTHLENTLDNTE 654
Qy 776 YRREVTYTLNFTSTYNISSITTVSCGRMAAPNTNCTCTGTDPDPDGSNTITSVHNKVV 835
Db 655 CREEVYTLNFTSTYNISSITTVSCGRMALPTOSTCTTGTDPDPDGSNTITSVHNKVV 714
Qy 836 KFSGFESASHGPIKAYAVILTTGEAGHPADVLKATYDDPFKAGADTYTYTLIRTEBKRS 895
Db 715 KFSGFESASHGPIKAYAVILTTGEAGHPADVLKATYDDPFKAGADTYTYTLIRTEBKRS 774
Qy 896 QSLSEVLKYEIDVGNESITLGYNGKLEPLGSYACVAGFTNITFHPOKGLDGAESYV 955
Db 775 QGISEALNTEIDVGNOSTTGLGYNGRLEPLGSYACVAGFTNITFYNQNDGLINDGESYV 834
Qy 956 SFSKSYDAVSLPDPBGVYICGAFVFCIRGALIVYVVGFTFPRKKRKAOKKNVSPSOIKP 1015
Db 835 SFSKSYDAVSLPDPBGVYICGAFVFCIRGALIVYVVGFTFPRKKRKAOKKNVSPSOIKP 894
Qy 1016 KKSGLIRVENEFAVFKQADNSCGFAEYEDLKLVGISOPRYAELAEKGRKRYNNVL 1075
Db 895 KKSGLIRVENEFAVFKQADNSCGFAEYEDLKLVGISOPRYAELAEKGRKRYNNVL 954
Qy 1076 PYDISRYKLSVQTHSTDDYINANYMPGYHSKDFIATQGPLNTLKDFWEMWMEKNVYAI 1135
Db 955 PYDISRYKLSVQTHSTDDYINANYMPGYHSKDFIATQGPLNTLKDFWEMWMEKNVYAI 1014
Qy 1136 IMLTCKYBQGRTKCEBYWPSQADYGDITYAMTSEIYLPBWTIRDFVYKRIQISEHPL 1195
Db 1015 VMLTKCYBQGRTKCEBYWPSQADYGDITYAMTSEIYLPBWTIRDFVYKRIQISEHPL 1074
Qy 1196 RQFHTSPDHGVDPDTDLINFRYLVDYMKOSPSPSPILVHGSAGVGTGTFIADRL 1255
Db 1075 RQFHTSPDHGVDPDTDLINFRYLVDYMKOSPSPSPILVHGSAGVGTGTFIADRL 1134
Qy 1256 IYQIENENTVDYVGIYVLDLRHMRPLMVQTEQYVFLNQCVLIDIVRSQKSKYDILYQNTT 1315
Db 1135 IYQIENENTVDYVGIYVLDLRHMRPLMVQTEQYVFLNQCVLIDIVRSQKSKYDILYQNTT 1194
Qy 1316 AMTIYENLAPYTTTGKTNGYTA 1337
Db 1195 AMTIYENLAPYTTTGKTNGYTA 1216

RESULT 5
08C1W9 PRELIMINARY; PRT; 1238 AA.
AC 08C1W9;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2004 (Tremblrel. 23, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Protein tyrosine phosphatase receptor-like protein J.
GN Name=Pcpj;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvS1;
RX MEDLINE=22084386; PubMed=12089527; DOI=10.1038/ng903;
RA van Mezel T., Ruttenkamp C.A.L., Zanon C., Straasen A.P.M., Vlcek C.,
RA Celkova T., Tripodis N., Groot P.C., Dauwerse H., van Ommen G.J.B.,
RA "Pcpj" is a candidate for the mouse colon-cancer susceptibility locus
RT Sccl and is frequently deleted in human cancers."
RL Nat. Genet. 31:295-300(2002).
DR EMBL: AY038877; AAN11409.1; -.
DR EMBL: AY038861; AAN11409.1; JOINED.
DR HSSP: P18052; 1YFO.
DR MGD: MGI:104574; Pcpj.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.

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DR GO: GO:0007507; P:heart development; IMP.
DR GO: GO:0001570; P:vasculogenesis; IMP.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; fn3; 6.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PRYPHPTASE.
DR SMART: SMO0060; FN3; 7.
DR SMART: SMO0194; PTPc; 1.
DR PROSITE: PS00853; FN3; 5.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PP; 1.
KW Hydrolyase; Receptor.
SQ
SEQUENCE 1238 AA; 136712 MW; DC294E254395B6C CRC64;

Query Match 63.8%; Score 4483.5; DB 2; Length 1238;
Best Local Similarity 66.9%; Pred. No. 1.2e-245;
Matches 897; Conservative 109; Mismatches 229; Indels 105; Gaps 12;

Qy 1 MKPAAERARLPSPSPGRLMALPLLLLRGLIACAGTSPSPDPSPVATVATGENGTQ 60
Db 1 MKPAAERARLPSPSPGRLMALPLLLLRGLIACAGTSPSPDPSPVATVATGENGTQ 43
Qy 61 ISSTAESFHQNGTQVETNNTSEDESSGANDSLTPPEGSGNTDGAOKTPSSTGPS 120
Db 44 ----- 43
Qy 121 PVFDKAVSISPTNVILTWKSNPTDPAEYKVVYHKKNEKTIIVHQPCNITGLRPA 180
Db 44 --FDIEAV-VSPISVLLTWKHNDSGASECR--IENKRESNLTFPVKQKTSNITGLSPGT 98
Qy 181 SYVFSITPFGIGNETGWDPRIYKVTPEIPVSDLRVALTYRKALSSNGKGTASRYLL 240
Db 99 SYTFSIISVTNTEINLK---TITTEPWPVSDLHTVSVGYQARLITWNNANGTASYML 154
Qy 241 ESIGSHEBLQDSSLQVNIISDLKPGVOYINPYLL--QSNKTKGDPGLTEGGLDASNTERS 299
Db 155 EELTTHS-----SVNISGLKPGTN--NSFAPPSNETIADPAVAEVPDANGTKRI 203
Qy 300 RAGSPFAPVHDESLVGPVDSGQGSQSDRTVELVGLGEGTRYNATVYSGAANGTEGQPOA 359
Db 204 PV-TNLSQLHKNSLVS-VDPSPGQDPSLTLEILTDLPDQYANATISQAANGTEGQPRN 261
Qy 360 IEFRTNALIYQFVDYVANISATSLTLIKVSDNESSNYTKIYHAGETDSNLANVSEBRA 419
Db 262 KVFETNSTQVSDVYANMISASMTLTKWSNYDGSRTSIYKIHVAGGTHSVNQTIVNTEEA 321
Qy 420 VIFGLASTFYNITVCGVLDIGTBPGLQVHPVSPDPRTVVSSTTEIGLAWSSHDA 479
Db 322 IILGLSSSTLVNITVHPFLQGTBGPFLQVYISPDQVSDPRVTVSTRALGLAMRSDS 381
Qy 480 ESPQMIHTQEGAGNSRVEITTNOSIIGGLFPGTKYCFEIVPKPNTTEGASRTVNCRTV 539
Db 382 KSEFIRFKQDGEGRHASTGNSYMWEDLKGSYHFEIIPRPDGTBGLSIVNSTD 441
Qy 540 PSAVFDIHVVYVTTTMMMLDKSPDGASEYVYHLVIESKGS-NHISTYDKAIILOGLIP 598
Db 442 PSAVTDIRVVNISTTEQMLEQNTDDASGYVHLVLESKGSIIRTNSSQKMITVGSITP 501
Qy 599 GTLVNITISPRVHVMDPRSTAQYTPSNVSNIDVSTNTTAATLSQNPDPDASPYSYC 658
Db 502 GTLVNITIFPEVDIIGISNSITQYTPSSVSHLEVNTTTTAATLRKMGNEPAASATAYS 561
Qy 659 LLIEKANSNATQVVT-DGITDATVTEILPGSSVYVEIFAQYGDGKISLEPRKSFCT 717
Db 562 VLIKTGDSGNVSNIFKPSI---LIPELIPGVSYVVLITVQGDGTTSLVPMNLFC 618
Qy 718 DPASMASPDCEVVPKPEPALVILKTCPPGANAQFLEVSGAMNNAHTLESSENGTEYR 777
Db 619 EPEVTSFHCCEVVPKPEPALVILKMACPCPGMYTGFEIGVRSDSWDMNTRLENCTSDDECR 678

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QY 778 TETVYLNFSSTSYNISTITVSCGMAAPRTNTCTTGTTDPPPPGSPNITSVSHNSVKYK 837
 DB 679 TEVAVYNFSTSYNISTATISCGMALPACONICTTGTTDPTDPSBNITSVSHNSVKYK 738
 QY 838 SCPEASHGPIKAYAVILTTGEAGHPADVLKTYTDDFKKASDIYVYVILIRTEKGRSQS 897
 DB 739 SCPEASHGPIKAYAVILTTGEAGHPADVLKTYTDDFKKASDIYVYVILIRTEKGRSQS 798
 QY 898 LSEVLKYEIDVGNESSTLGYNGKLEPIGYSYACVAFGNITFPHQNGLLDGLASYSYF 957
 DB 799 LSEVLKYEIDVGNESSTLGYNGKLEPIGYSYACVAFGNITFPHQNGLLDGLASYSYF 858
 QY 958 SKYSDAVSLPDDPGVTCGAVFCIGALVITVGGFIEMFKKKKAKNNVSPSOIKPKK 1017
 DB 859 SPYSEAVFLPDDPGVTCGAVFCIGALVITVGGFIEMFKKKKAKNNVSPSOIKPKK 918
 QY 1018 SKLIRVENFEAFKQKQADNSNGCFABEYEDLVLGISOPTKAAELAEKNNKNNVLPY 1077
 DB 919 SKLIRVENFEAFKQKQADNSNGCFABEYEDLVLGISOPTKAAELAEKNNKNNVLPY 978
 QY 1078 DISRYVLVQTHSTDDYINANMPGYSKQDPIATQGPLPNTLKDFMFMWMEKNNVYALIM 1137
 DB 979 DISRYVLVQTHSTDDYINANMPGYSKQDPIATQGPLPNTLKDFMFMWMEKNNVYALIM 1038
 QY 1138 LTKCVQEGRTKCEEYWPSSKQADYDITVAMTSEIPLPEMTIRDPYVNIQTSSEHPJRO 1197
 DB 1039 LTKCVQEGRTKCEEYWPSSKQADYDITVAMTSEIPLPEMTIRDPYVNIQTSSEHPJRO 1098
 QY 1198 FHFSTWPHGVPDPTDILINFRYLVRDWMKQSPESPILLVHCSAGVGTGPIADRLIY 1257
 DB 1099 FHFSTWPHGVPDPTDILINFRYLVRDWMKQSPESPILLVHCSAGVGTGPIADRLIY 1158
 QY 1258 QIENENTVAVYGIYVDLREMRPLAMVQTEDOYVFLNQCVLDIRSQKSDKVLIIYONTAM 1317
 DB 1159 QIENENTVAVYGIYVDLREMRPLAMVQTEDOYVFLNQCVLDIRSQKSDKVLIIYONTAM 1218
 QY 1318 TIYENLAPVTTFGKTNGYIA 1337
 DB 1219 TIYENLAPVTTFGKTNGYIA 1238
 RESULT 6
 Q6P4H4 PRELIMINARY; PRT; 539 AA.
 AC Q6P4H4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE PTPRJ protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Ditchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Klausner R.;
 RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063417; AA063417.1;
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR Pfam; PF00041; fn3; 4.
 DR SMART; SMO0060; fn3; 4.
 DR PROSITE; PS00853; FN3; 3.
 SQ SEQUENCE 539 AA; 57189 MW; E970DA55A6B2E3BD CRC64;
 Query Match 39.6%; Score 2784; DB 2; Length 539;
 Best Local Similarity 99.8%; Pred. No. 1,le-149;
 Matches 537; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKPARBARLPKPSGRLMALPLILLRLGLQIICAGCTSPIDPSVATVATGNGITQ 60
 DB 1 MKPARBARLPKPSGRLMALPLILLRLGLQIICAGCTSPIDPSVATVATGNGITQ 60
 QY 61 ISSFAEFHONGGTPOVETNTSEDESSGANDSLRTPGSGNGTGAOKTSSSTGPS 120
 DB 61 ISSFAEFHONGGTPOVETNTSEDESSGANDSLRTPGSGNGTGAOKTSSSTGPS 120
 QY 121 PVFDIKAVSISPTNVLITWKSNDTPAEEYKYVYKHKNENKITTIVHQPCNITGLRPAT 180
 DB 121 PVFDIKAVSISPTNVLITWKSNDTPAEEYKYVYKHKNENKITTIVHQPCNITGLRPAT 180
 QY 121 PVFDIKAVSISPTNVLITWKSNDTPAEEYKYVYKHKNENKITTIVHQPCNITGLRPAT 180
 DB 121 PVFDIKAVSISPTNVLITWKSNDTPAEEYKYVYKHKNENKITTIVHQPCNITGLRPAT 180
 QY 181 SYVSTITPGIGNETWGPRIYKTYTTEPIPIVSDIRVALTGRKAAALSMNGNGTASCVL 240
 DB 181 SYVSTITPGIGNETWGPRIYKTYTTEPIPIVSDIRVALTGRKAAALSMNGNGTASCVL 240
 QY 181 SYVSTITPGIGNETWGPRIYKTYTTEPIPIVSDIRVALTGRKAAALSMNGNGTASCVL 240
 DB 181 SYVSTITPGIGNETWGPRIYKTYTTEPIPIVSDIRVALTGRKAAALSMNGNGTASCVL 240
 QY 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLQSNKTKGDPLEGGGLDASNTFSR 300
 DB 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLQSNKTKGDPLEGGGLDASNTFSR 300
 QY 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLQSNKTKGDPLEGGGLDASNTFSR 300
 DB 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLQSNKTKGDPLEGGGLDASNTFSR 300
 QY 301 AGSPFAPVHDESLVGPVDPSSGOQSRDTEVLVGLBGTGYNNATVYVSOANGTEGPOAI 360
 DB 301 AGSPFAPVHDESLVGPVDPSSGOQSRDTEVLVGLBGTGYNNATVYVSOANGTEGPOAI 360
 QY 361 BFRNALQVDFDAVAVNISATSLTIWKVSDNESSNTYKIHVAGETDSSNLVSEPRAY 420
 DB 361 BFRNALQVDFDAVAVNISATSLTIWKVSDNESSNTYKIHVAGETDSSNLVSEPRAY 420
 QY 361 BFRNALQVDFDAVAVNISATSLTIWKVSDNESSNTYKIHVAGETDSSNLVSEPRAY 420
 DB 361 BFRNALQVDFDAVAVNISATSLTIWKVSDNESSNTYKIHVAGETDSSNLVSEPRAY 420
 QY 421 IPGLRSTFYNIITVCPVLGDIIEGTPGLQVHTPPVPSDPRVYVSTTEIGLAWSSHDAE 480
 DB 421 IPGLRSTFYNIITVCPVLGDIIEGTPGLQVHTPPVPSDPRVYVSTTEIGLAWSSHDAE 480
 QY 481 SFQWHTIQEGAGNSRVEITTNOSITIGLFPGRKYCEIYKPKPNGTGASRTVCNRT 538
 DB 481 SFQWHTIQEGAGNSRVEITTNOSITIGLFPGRKYCEIYKPKPNGTGASRTVCNRT 538
 RESULT 7
 Q9W6V5 PRELIMINARY; PRT; 1406 AA.
 AC Q9W6V5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Supporting-cell antigen precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxId=9031;
 RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=99296852; PubMed=10366616;
RA Kruger R.P., Goodyear R.J., Legan P.K., Marchol M., Raphael Y.,
RA Cocanache D.A., Richardson G.P.;
RT "The supporting-cell antigen: a receptor-like protein tyrosine
phosphatase expressed in the sensory epithelia of the inner ear.";
RL J. Neurosci. 19;4815-4827(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RA Legan P.K.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238216; CAB41885.2; -.
DR HSSP; P18052; IYFO.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_EP.
DR Pfam; PF00041; FN3; 8.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PRO0700; PHYSPHATASE.
DR SMART; SM00060; FN3; 9.
DR SMART; SM00194; PTPc; 9.
DR PROSITE; PS00853; FN3; 9.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KM Hydrolase; Signal.
FT SIGNAL 1 24 Potential.
SQ SEQUENCE 1406 AA; 154213 MW; 2D609885CC0F367B CRC64;
Query Match 39.2%; Score 2752.5; DB 2; Length 1406;
Best Local Similarity 45.7%; Pred. No. 2.9e-147;
Matches 624; Conservative 169; Mismatches 459; Indels 112; Gaps 35;

Db 545 MWND-----TASDYTYRIEVRNGHSVNNKTSNIPEITGLNPGCLVTTFAVAA 596
Qy 525 NG-TEGASRTVCNRVTSADFVDFHVVYVTTTMMWLDKSPD-GASEYVYHLVIESKGS- 581
Db 597 DGETEGGASISVYTKRAVLAHLKTEVGVTSVNLTVNDTDSASTYR-IEVRNGSS 654
Qy 582 -NHTSTYDAKATLQGLIPGLTYNTTISPEV-DHVMGDNSTAQYTPRSVNSIDVSTN 637
Db 655 INNKTSDITDA-EITGLDPTGLYFTFAVAADQGTAGEGASISLYTKPSVNLKAEVY 713
Qy 638 T-TAATLSWQNFDDASTYSCYLIEKAGNS-SNAQVVDIGITDATTVELTIGSSYTV 695
Db 714 TMTSVNLTMWVNAESASYT-RIEVAHSLINETM-----SNVTKSIYVLLIPGTSYNF 767
Qy 696 EIFAQVDDGKISLEPGKSFCTDPASMASPCEVVPKPAVLKMTCPGANAGFELEVS 755
Db 768 TVPFAADNQTGEGASISQNTYPPSSVNAQCEAVNAMSITLTKMCPYGGYSFDEIF 827
Qy 756 SGAMNNAATHESGSENGTE-YRTEVYTLNFTSYNISTTVSCGMAAPRNTCTTGIT 814
Db 828 NGTWTKKQGFQGRGSESEIFKTEP-LDYKYTYVSVTVSDGLTSLPVQIKICTSIT 885
Qy 815 DPPPDGSPNITSYSHNSVKKSGFEASGPIKAYV-ILTTGAGHPADVLKTYDD 873
Db 886 DPVPNKAPLVKAVSHNSLSVEFPDFESVNGPLKAYAVMTVEAGCLPSKSDLDYTYND 945
Qy 874 FKGAADTYTYLIRTEKRSOSLSVLYKEIDVNGSEITLGYNGKLEPLGSRACVA 933
Db 946 FKQMTATVYTYVLDVEIS-SSSHSQNHNIYDVGNMTYGENPPLPLSHSTRASVA 1004
Qy 934 GFTNITFHPONKGLIDAESYVSFSRYSDAVSLPQDPGVI CGAVFGCIFGALVITVVG 993
Db 1005 GFTNITVANK--IMEQSVSFSPCSEVSLPQDPGVLAGAVIGCLAILAVVALGY 1062
Qy 994 IFWRKKKADNNEVSSQIKPKSKLIRYENFAFYKKQADNSCGFAEYEDLKVGI 1053
Db 1063 IFWRRRKDKRNEVSSPIKIKSKMIKYENFESYKKQADNSCGFAEYEBELKAGV 1122
Qy 1054 SOPKYAEIAENGNKNVNLPPDISRVKLSVQTHSTDDYINANNVPGYHKKDFIATQ 1113
Db 1123 HQPFAEIAENKKNVNLPPDISRVKLSNPSCTTDDITANNVPGYSSKKAFLAAQ 1182
Qy 1114 GPLPNTLKDFWRMWEKNVYAIIMLTLCVEGRTKCEYMPSPKQADYGDITVAMTSEIV 1173
Db 1183 GPLPNTIEDFRMIMWENKISYIWLTKVCGARTKCGQYMPDKSKSYGDIIVTMVEEV 1242
Qy 1174 LPEWTIDFTYKNIQISESHPLRFHFTSPDHGVPDTDLLINFRYLVRDYKQSPES 1233
Db 1243 LPEWTIDFVVENADTWESHVFOFHFTSPDHGVPDTDLLINFRHLVHEYSQNPIDS 1302
Qy 1234 PIIVHCSAGVGRCTFLAIDRLTYQIENENTVDYGI VYDLMRMRPLMVQTEDDGYFLNQ 1293
Db 1303 PIIHCSAGVGRCTFLAIDRLTYQIENENTVDYGVVYDLMRMRPLMVQTEDDGYFLNQ 1362
Qy 1294 CVLIDIVRSQDSKVDLIYQNTTAMTIYENLAPVTFPGTKGYIA 1337
Db 1363 CVMIDIHSQKEKKTDLTYQNTTAMTIYENFTPGAFPKANGYHA 1406

RESULT 8
Q9NPRS PRELIMINARY; PRT; 425 AA.
AC Q9NPRS;
ID Q9NPRS;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PTRR; protein tyrosine phosphatase receptor J, eta (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Aulfray C., Anseorge W., Ballabio A., Estivill X., Gibson K.,
 RA Lehrach H., Poustka A., Lundeberg J.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Andreu N., Estivill X., Escarceller M., Sumoy L.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ359057; CAB94390.1; -
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS00853; FN3; 1.
 DR Receptor.
 FT NON TER 425 425
 SQ SEQUENCE 425 AA; 45078 MW; BD1ACASD345B7027 CRC64;
 Query Match 31.1%; Score 2184; DB 2; Length 425;
 Best Local Similarity 99.8%; Pred. No. 8.7e-116;
 Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKPARAEALPPRSPGLRWALPILLILALGQILCAGGPRSPIDPSVATVATGNGITQ 60
 DB 1 MKPARAEALPPRSPGLRWALPILLILALGQILCAGGTPSPIDPSVATVATGNGITQ 60
 QY 61 ISSVASFHKQNGTGTPOVEINTSEDESSGANDSLRPEQSGNGTDGASOKTPSSTGPS 120
 DB 61 ISSVASFHKQNGTGTPOVEINTSEDESSGANDSLRPEQSGNGTDGASOKTPSSTGPS 120
 QY 121 PFEDIKAVSISPTNVLITWKSNDTAASEKYVYVHKHMEKITTIVHQPWCNITGLRAT 180
 DB 121 PFEDIKAVSISPTNVLITWKSNDTAASEKYVYVHKHMEKITTIVHQPWCNITGLRAT 180
 QY 181 SYVFSITPGIGNETWGDPRVIVITEPIPVSDLRVALTGVRKAALSMNGNGTASCRVL 240
 DB 181 SYVFSITPGIGNETWGDPRVIVITEPIPVSDLRVALTGVRKAALSMNGNGTASCRVL 240
 QY 241 BSIGSHEELTQSRQVNIISDLKPGVQVNIINPYLLQSNKTKGDPITGEGIDASTESR 300
 DB 241 BSIGSHEELTQSRQVNIISDLKPGVQVNIINPYLLQSNKTKGDPITGEGIDASTESR 300
 QY 301 AGSPAPVHDESLVGPVPSGQSRDTEVLLVGLPGRVNAVATYSGAANGTSGQPAI 360
 DB 301 AGSPAPVHDESLVGPVPSGQSRDTEVLLVGLPGRVNAVATYSGAANGTSGQPAI 360
 QY 361 EFRINAIOVFDTAVNISATSLILIMKVSNDNESSNTYKLIHAGETDSSMLANSEPRAY 420
 DB 361 EFRINAIOVFDTAVNISATSLILIMKVSNDNESSNTYKLIHAGETDSSMLANSEPRAY 420
 QY 421 IPRGLR 425
 DB 421 IPRGLR 425
 RESULT 9
 Q61373 PRELIMINARY; PRT; 361 AA.
 ID Q61373
 AC Q61373;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Protein tyrosine phosphatase (Fragment).
 GN Name=Prtp; Synonyms=Prp-RI9;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57/BL6; TISSUE=Liver;
 RA Higashitsuji H., Arai S., Furutani M., Imamura M., Kaneko Y.,
 RA Takenawa J., Nakayama H., Fujita J.;

RT "Enhanced expression of multiple protein tyrosine phosphatases in the
 RT regenerating mouse liver: Isolation of prp-rl 10, a novel
 RT cytoplasmic type phosphatase with sequence homology to cytoskeletal
 RT protein 4.1." (1995).
 RL Oncogene 0:0-0(1995).
 DR EMBL: D49393; BAA08386.1; -.
 DR HSSP: P18052; IYPO.
 DR MGD: MGI:104574; Prtpj.
 DR GO: GO:0005615; C:intracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0007507; P:heart development; IMP.
 DR GO: GO:0001570; P:vascularogenesis; IMP.
 DR InterPro: IPR00387; TYR phosphatase.
 DR InterPro: IPR00242; TYR PP.
 DR Pfam: PF00102; Y phosphatase; 1.
 DR PRINTS: PR00700; PRTPPHRTASE.
 DR SMART: SM00194; Prtp; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PP; 1.
 DR Hydrolyase.
 FT NON TER 1 1
 SQ SEQUENCE 361 AA; 41726 MW; B51462B8D11023A4 CRC64;
 Query Match 26.3%; Score 1847; DB 2; Length 361;
 Best Local Similarity 94.7%; Pred. No. 9.2e-97;
 Matches 342; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 977 VFQIGRALYIVYVGGIFFRKKRKADKANNVFSQIKPKSKLIRVENFEAYFKQOAD 1036
 DB 1 VFQIGFALAITVGGIFFRKKRTDKANNVFSQIKPKSKLIRVENFEAYFKQOAD 60
 QY 1037 SNCGFAEEYEDLKLVGISQPKYAAELAENRGNKRYNNVLPYDISRYKLSVQSTSDYIN 1096
 DB 61 SNCGFAEEYEDLKLIGSLKTAELAKRGNKRYNNVLPYDISRYKLSVQSTSDYIN 120
 QY 1097 ANTWPGHSGKDDIATQGLPNTLKDFWRVWMEKNVYAILMLTKCYEQGRTKCEYWPSS 1156
 DB 121 ANTWPGHSGKDDIATQGLPNTLKDFWRVWMEKNVYAILMLTKCYEQGRTKCEYWPSS 180
 QY 1157 QAQDYGDIYAMTSEIYLPMTIRDTLVKNIGQSESHPRQPHFTSWPHGVPDITDLI 1216
 DB 181 QAQDYGDIYAMTSEVYLPMTIRDTLVKNIGQSESHPRQPHFTSWPHGVPDITDLI 240
 QY 1217 NFRYLVDYKQSPSPSPILVHCSAGVGTGFIAIDRLIYOIENENTVDVYGIYDLDM 1276
 DB 241 NFRYLVDYKQSPSPSPILVHCSAGVGTGFIAIDRLIYOIENENTVDVYGIYDLDM 300
 QY 1277 HREPLMOTEDQYVFLNQCVLIDVRSQDSKVDLIYONTTAMTIYENLAFTTGGKTNGYI 1336
 DB 301 HREPLMOTEDQYVFLNQCVLIDVRSQDSKVDLIYONTTAMTIYENLAFTTGGKTNGYI 360
 QY 1337 A 1337
 DB 361 A 361
 RESULT 10
 Q8CIW2 PRELIMINARY; PRT; 1998 AA.
 ID Q8CIW2
 AC Q8CIW2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Vascular endothelial protein tyrosine phosphatase.
 GN Name=Prtpb;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster;

RX MEDLINE=22220060; PubMed=12234928; DOI=10.1093/emboj/cdf497;
 RA Navoroth R., Poell G., Ranft A., Klope S., Samulowitz U., Fachinger G.,
 RA Golding R., Shima D.T., Deutsch U., Westwieser D.;
 RT "ye-ppp and ve-cadherin ectodomains interact to facilitate regulation
 RT of phosphorylation and cell contacts.";
 RL EMBO J. 21:4885-4895(2002).
 DR EMBL; AY077755; AAL75813.1; -.
 DR HSPB; P18052; 1YFO.
 DR MGD; MGI:97809; Pcpb.
 DR GO; GO:0016787; F:Hydrolase activity; IEA.
 DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR000187; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00041; fn3; 15.
 DR Pfam; PF0102; Y_phosphatase; 1.
 DR PRINTS; PRO0700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 16.
 DR SMART; SM00194; PTRG; 1.
 DR PROSITE; PS00853; FN3; 15.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
 DR HydroLase.
 KW SEQUENCE. 1998 AA; 224474 MW; B37EA6501EF03B5D CRC64;
 SQ
 Query Match 17.9%; Score 1259.5; DB 2; Length 1998;
 Best Local Similarity 28.8%; Pred. No. 3e-62;
 Matches 378; Conservative 216; Mismatches 500; Indels 217; Gaps 45;

QY 104 NGTGAASQKTSSTGSPSPVPDIKANISIPVIVILTKMSNDPAAASYKVVHMKMENKTI 163
 DB 805 SGQYEAASQGTGRITPEVPKDLTLNRTSTEDLHVMSFANEDVDYE--VQLFDMKVF 862
 QY 164 TVVHQPMCNITGLPATSYVF-SIRPG-----IGNETWGDPR--VIKITEPIVSDLR 214
 DB 863 PHIL-----VMTATEYKFTALTRGRHKYILVLTISGDVQASFIIGLVPSTVVKIH 915
 QY 215 VALTGVK-KAALISWNGNGTASCRVLLESIGSHLELTODSRLQVNI SLPKGVQVNIINPY 273
 DB 916 ISANGATRLMTVMSPPGG-----DVDSY 939
 QY 274 LLOGNKTKGDELGTBEGGLDASNTERSRAGSPAPVHDSLVGPVDPSSGQGSRDTEVLV 333
 DB 940 VVSAFR-----ODEKVSQTIPIR-----ASEHTFH 965
 QY 334 GLEPGTRYNATVYVSOANGTEGQPOAIEFRITNAIOVPVTAVN-ISAATSLTIWKVSDNE 392
 DB 966 RLEAGAKTRIAIVS-VSGSLNQIDALG-QIVPASVQGVANANVSSSLVTSWQKALGV 1023
 QY 393 SSSNVTYKIHVAGETSSNLNVSEPR-----VIFGLSSTFYNTVTCPEVLGDIETG 444
 DB 1024 AE---RYDILLNENGLLSNVSEBAPARQHKFEDLTGPKG---YKQOILTVSGGLPSK 1076
 QY 445 PCFLQVHTPPVPVSDFRTVAVSTTEIGLMSHDSQMI---TQSGAGSRVEI-TT 500
 DB 1077 ESQAEGRTVPAVNTLRTITENSSRLSGMTASBGLSWYNIPLVNPRTLOERAQVDPL 1136
 QY 501 NQSIIGGLFGTKTCFEIVPKPGNGTEGASRTVCRVTPSAVPDIHVYVYVTTT-MMLD 559
 DB 1137 VQSFSGVLLQGRYKVIYTH--SGELSNESFICRGRIVPAVNVHLKSHNTDLSLWFS 1194
 QY 560 WSPDGAEEYVHVLVESKSGNSHTSYDKAIT--LQGLIPG--TLNNTITSPEDVH 613
 DB 1195 WSPASGDDP-YELLVYNPNGTKENMKKEKDETEWRFGQLVGRKXTLLVYVTHSGDLNKK 1253
 QY 614 WGDPRSTQYTRPSNVNIDVSTNTATL---SMQFPDAS---PTYSCLILIEKAG 665
 DB 1254 VTGEGRTVP-SPPSLSPADVANTSLATWKGPPMTWYVPELQWFGDALITFNYPSS 1312
 QY 666 NSSNATQVVTDIGITDAVTELLIPGSSYTVVEIFAQVGDGIXSL-BPGRKSFCTDPASMAS 724

DB 1313 RKSEG-----RIVGLHGRSYQSFVKTVSGDSWMTYKSPISGSVRYTPDKIQN 1361
 QY 725 FDCVVPKEPALVUKTCPCPPANANGFELEVSSGAMNNAATHLESSESGTEYRREVTYLN 784
 DB 1362 LHCR-PONSTAIACSWLPDPSDFGYSIE-----CRKDDTEIEFSRLKEKESILN 1412
 QY 785 F-----STSYNISITVYSCGMAAPTNTCTTGITDPPPDGSDNI-----TSVSHNSV 833
 DB 1413 IMLVPHKRYLVSTIKVGSAGTSEVEDSTITMIDRRPQP--PHIRNKEVDLISKSSI 1470
 QY 834 K-VKSGFEASHGPITAVAVILTTG-----EAGHPADVLYKTYVDFKKAASDTYV 883
 DB 1471 NFTVNCWSFSDTNGAVKFAVAVREADSMDELKPEQGHPLPSYLEYRHNASIRVQTVY- 1529
 QY 884 TYLIRTEKGRSQSLSEVLKKEIDVGNESITLG-----YNGKLEPIGSTRACAG 934
 DB 1530 -FASKCAESPSSSKS-----FNILGAEMLSGKCKDPSQOKFDDGLKPTAARISIRA 1584
 QY 935 FTNITFPHQNGKLDGABSVYFSRYSDAVSLPQDP--GVICGAVFGCIFGALVIVTVGG 992
 DB 1585 FTQLP-----DEDLKEFTKPLYSIDTPPSPMTTSESEPLFGVIEGVSAGLFLIGMLVALVAF 1640
 QY 993 FIFWRK--KRDANKNEVSFSQIR-----KSKSLRVENFEAYFKQQAQS 1037
 DB 1641 FICRQKASHSRERSARLSIRDRPLSVHNLGQKGRKTCSPIKINGFEHFMKLQADS 1700
 QY 1038 NCGFAEVEDLKVIGISOPKFAELAEKGRNRNNVLPYDISVKLS-VQTHSTDQYIN 1096
 DB 1701 NYLLSKVEDLKDQGRSQCDIALPERGRNRYNNLIPYASRVKSNVDDPCSDYIN 1760
 QY 1097 ANYMPGYSKDPFATOGPLPNTLKDFFRWYMEKNVYAIIMLTVCVEQRTKCEYMPSK 1156
 DB 1761 ASYIPGNFRREYIATGCPLEGTODFRKAMQEQNHIVAVTQCVBGRKCHQYVAD 1820
 QY 1157 Q-AADYGDITVAMTSBIYLPWTIRDTFTVKNIIQTSSEHPL-RQPHFTSWPDHGVPTDIL 1214
 DB 1821 QDPLYYGDLILQWSESVLPFWTIRBFKICSEBQDLAHRILRHFTYVWPDHGVPTQS 1880
 QY 1215 LINFRILVRYDMKQSPESPFLVHCSAGVGTGTFIALDRLIYQLENNTYVDVGIYVDL 1274
 DB 1881 LIQFRTVRYDYINSFGAGPFWVHCSAGVGTGTFVALLDRILQQLDSQSDVADIGAVHDL 1940
 QY 1275 RMHRPLWQTEQDYVPLNQCLDIVRSQKSDVLDIYQNTAMTYENLAP 1325
 DB 1941 RLHRYVMQVTECYVYHLQCVRDVLRKGLRN---EQENLPLFIYENVP 1987

RESULT 11
 PTPB_HUMAN
 ID PTPB_HUMAN STANDARD; PRT; 1997 AA.
 AC P23467;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein-tyrosine phosphatase beta precursor (EC 3.1.3.48) (R-PTP-beta)
 GN Name=PTPB; Synonyms=PTPB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=9106018; PubMed=2170109;
 RA Krueger N.X., Streuli M., Saito H.;
 RT "Structural diversity and evolution of human receptor-like protein
 RT tyrosine phosphatases";
 RL EMBO J. 9:3241-3252(1990).
 CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

QY 819 PDGSPNI-----TSVHNSVK--VKFSGFEASHGPIKAAVAILTTG-----EAGHP 862
 DB 1451 P--PPIHIVNEKVLISKSSINFTVNCWSGSDTNGAKVFTVVRADSGDELKPEQHP 1508
 QY 863 SADVLKTYTDDFKKASDVTYVTLIRTEKGRSQSLSEVLKYEIDVNESTTLG----- 916
 DB 1509 LPSELYEVRHNASIRVQNTN--FASKCAENPNSNKS-----FNKLGAEMESLGCKDPT 1562
 QY 917 ---YNNKLEPPLSYRACVAGFTNITHPQNGKIDGAESEVSR--YDA-VSLP--- 967
 DB 1563 QOKFCDDPLKPHAYRISIRAFQ-----LFD--EDLKEFTKPLYSDFPFLPTT 1611
 QY 968 -ODPGVIGAVFGCIFGALVI---VTVGFIWFRK--RDKAKNNEVSQIRP----- 1015
 DB 1612 ESEB--LFGAIEGVSAGLFLIGMLVAVALICQKSHGERSALSTRDRPLSVHL 1669
 QY 1016 -----KSKLIRVENFEAYFKQQAQDSNCGFAEEYEDLKVGISQPKYAEALENRG 1067
 DB 1670 NLGQKGRKTSCTSPKINQFEGHFMKLQADSNYLLSKYEELKQVGRQSCDIALPENRG 1729
 QY 1068 KKNYNNLTPYDISRVKLS-VQTHSTDYINANNPQSHSKDPFATQGLPNTLKDFWRM 1126
 DB 1730 KNRNNNLTPYDARTKSNVDDDCSDYINASYIPGNFRREYLVQGLPEGTQDDPKM 1789
 QY 1127 VMEKNVYAILMTFCVEQGRKCEBYWPSKO-AQDYGDITVAATSEIYLPFWTIRDTYK 1185
 DB 1790 VMEONVNIWVTVQCVKGRKCDHYFPADDSLYTGDLIQMSSEVLSEMTIREKIC 1849
 QY 1186 NIQTSHP--ROFHTSWPDHGVPTDILLINRYLVDRYKMSPPSPILVHCSAGV 1244
 DB 1850 GEEOLDNRHLRHHYTPWPHGVETTSOLIGFVRTRDYINPSGAFVTVHCSAGV 1909
 QY 1245 RTGFTFIDLILYIENENTVYGIYDILMRHPLVQTEDEVPLNQCCLDIVRQKD 1304
 DB 1910 RTGFTFIDLILYIENENTVYGIYDILMRHPLVQTEDEVPLNQCCLDIVRQKD 1969
 QY 1305 SKVDLIYQNTAMTYENLAP 1325
 DB 1970 RS----EQENPLPPIYENVNP 1986

RESULT 12
 OGMZF6 PRELIMINARY: PRT: 1956 AA.
 ID OGMZF6
 AC OGMZF6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686E13109 (Fragment).
 GN Name=DKFZp686E13109;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN
 RP SOURCE FROM N. A.
 RC TISSUE=Human fetal kidney;
 RG The German Human cDNA Consortium;
 RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
 RA Han W., Wiemann S.;
 RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BX648771; CA646198.1; -
 DR HSSP: P18031; IKAV.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004745; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR008957; FN.III-like.
 DR InterPro: IPR003595; PTC_motif.
 DR InterPro: IPR00387; TYR_phosphatase.
 DR InterPro: IPR00242; TYR_PP.
 DR Pfam: PF00041; fn3_14.
 DR Pfam: PF00102; y_phosphatase; 1.

DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 16.
 DR SMART; SM00194; PTPC; 1.
 DR SMART; SM00404; PTPC_motif; 1.
 DR PROSITE; PS50853; FN3; 15.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
 DR KX Hydrolase; Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 1956 AA; 219892 MW; 0BEC5C8FAP17221B CRC64;
 Query Match 17.6%; Score 1239; DB 2; Length 1956;
 Best Local Similarity 29.6%; Pred. No. 4,2e-61;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
 QY 123 PDKAVISPTNVLTKWSDTAASEYKVKHNEKTTIVVHQPWCNITGLRPATSY 182
 DB 718 FDHYEVTIKKNKNNFIQTQKIP-----KSENE-----CVFVQVLPGRLY 755
 QY 183 VFSITPGIG---NETWGDPRVILKITEPIVSGDLRVALLGVKKAALSWNGNGTASCRV 238
 DB 756 SVTVTKSGQYEANEO-GNGRTI---PEPVKDLTRNRSSTEDLHVTVSGANG----- 803
 QY 239 LLESIGSHE--ELTQDSRL-----QVNIIDLKPGVQY-----NINPYLLQSNKT 280
 DB 804 ---DVQYELQLFNDMKVPPPHLVNTATEYRFTSLTPRQYKILVLTISGDVQSAFI 860
 QY 281 KG-----DPLG-----TEGGLDASN-----TERSPAGPTAPVHDESL 313
 DB 861 EGFVPSAVKNIHISPGATDSLTVMWTPGCGVDVSYTSAFHSQKVDQITPKH---- 916
 QY 314 VGPPDPSSGQSDTEVLVGLERGTFRYNATVYSGANGREGQPAIEFTNMIQVDPVT 373
 DB 917 -----VFETFRHLEAGEQYQIMAS--VSGALKQOINVAGRTVPASVQCVI 961
 QY 374 AVN-ISATSLTLIMKVSNDNESSNYTKIHVAGETSSNINVESEPA-----VIPGL 424
 DB 962 ADNAKSSYSILVNMQKAGVAB--RDILILLENGILLANTSEPAATKHKPEDLIPGK 1018
 QY 425 RSTFTYNTVCPVLGDIETGPGFLQVHTPPVPVSDFFRVTVVSTTEIGLAWSHDASEFQM 484
 DB 1019 K---YKIQILTVSGGLFSKQAQTEGRVPAAVTDLRTENSTFHLSPFTASGEISLWY 1074
 QY 485 HI---TOEGAGNSRVEL-TTNGSIIIGLFPQTKYCEIYPKPQNGTEGASRTVCNTPV 540
 DB 1075 NIFLYNDGMLOBAQVDPVQSPSPQNLQGRMYKXVIVTH--SGELSNESFTFGRTVP 1132
 QY 541 SAVFDIHVVVVTYTE--WMLDMKSPDGASEYVHLVIESKHSNHTSTYDRAIT---LQGL 596
 DB 1133 ASVSHLRGSRNRTTDSLMFNMSPASGDFP-YELLILNPNQGTKEKMKDLDLEWRFQGL 1191
 QY 597 IPGTLNITTSPEVDHVGDPNSTAQYTR-----PSNVSNIDVSTNTTAATL---SWON 647
 DB 1192 VPGKRYLVAV---VTHSGDLSNKVTASRTAPSPSILMSPADIANSTLAIATWKGPPDWT 1248
 QY 648 FDDASPTV---SYCLIEKAGNSNATQVYTDIGITATYTELIPGSSYVEIFAQVGDG 704
 DB 1249 YNFELQMLPRDALTYNPNYNNKSEGRIVYG-----LRPGSYSONVNTVSGDS 1298
 QY 705 IKSL-EPGRGSFCTDPASMASPCEVVPKPEPALVLKWTCPGANAGLEEVSSGAMNAT 763
 DB 1299 WKTSKRIIPGSVTKPKIQNLHCR-PQNSTALACSMIPDPDSDDGYSIE-----CR 1349
 QY 764 HLESCESENGTEKRTETVYINF-----STSYNISITTVSCGKMAAPFRNTCTGTIDPP 818
 DB 1350 KMDQVEYEFKRLKEKESLNLIMMLVPHKRYLVSIKVQSGAMTSEVEDSTIITWIDRPP 1409
 QY 819 PDGSPNI-----TSVHNSVK--VKFSGFEASHGPIKAAVAILTTG-----EAGHP 862
 DB 1410 P--PPIHIVNEKVLISKSSINFTVNCWSGSDTNGAKVFTVVRADSGDELKPEQHP 1467
 QY 863 SADVLKTYTDDFKKASDVTYVTLIRTEKGRSQSLSEVLKYEIDVNESTTLG----- 916

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DB 1468 LPSYLEYRHNASIRVQTVY--FASKCVENPNNSKSKS-----FVTKLGAMESLGGKCDPT 1521
QY 917 ---YVNGKLEPLGSYACVAGFNITFEHQNKGLIDGASYSFSR--YSDA-VSLP--- 967
DB 1522 QQKFCDDPLKPHNTAIVSTRALFQ-----LFD--BDLKEFKPLSLDFFSLPTTT 1570
QY 968 -ODPGVICAVFGCLFGALVI---VTVGGFIEMRK--RKDAKNNEVSFSQIKP----- 1015
DB 1571 ESEF--LFGALIEGVSAGLFLIGLVAVALLCROKVSIGRRRPARSLIRDRPLSYHL 1628
QY 1016 -----KSKLIRVENFEAFKKQADSNCGFAEEYDLKLVGISQPKYAAELANRG 1067
DB 1629 NUGQKNRRTSCPIKINQPEGHEFMKLQADSNVLSKEVEELDVARNQSCDIALPENRG 1688
QY 1068 KRRYNNVLPYDISRVKLS-VQTHSTDDYINANVMGYSKSKQFIATQGLPTLMDPFM 1126
DB 1689 KRRYNNILPYDATRYKLSNVDDPQSDYINASYSIFGNRRREYIVTQGLPETKDFMWM 1748
QY 1127 VKEKNVYALIMLTCEVQGRTECEEYWPBQ--ADYGDITVAMTSEIYLPWTITRDTVK 1185
DB 1749 VWEQVHNIVMTQCEVKEGRVACDRYWPADQDSLKYGDLILQMLSESVLPWTITREFKIC 1808
QY 1186 NQTESHPL-RQFHFTSWPDHGVPTDILLNFYLVVDYKQSPSPSPILVHCSAGVG 1244
DB 1809 GEEQLDAHRLIRHFHYTVPDHGVPEPTQSLIQFRTVADYINRSBGAPTVHCSAGVG 1868
QY 1245 RTGFTIALDRLIYQIENENTVDVYGIYVYDLRMHREPLMOTEDQYVFNOCVLDIYRSOKD 1304
DB 1869 RTGFTIALDRLIYQIENENTVDVYGIYVYDLRMHREPLMOTEDQYVFNOCVLDIYRSOKD 1928
QY 1305 SKVDLIYQNTTAMTYENLAP 1325
DB 1929 RS-----EQENLPEFYENVNP 1945

RESULT 13
AC Q80VN7 PRELIMINARY; PRT; 1102 AA.
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ptpdb protein (Fragment).
GN Name=Ptpdb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=NMRI; TISSUE=Mammary tumor;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarake P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimoldi J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.B., Scherch A., Schein J.E.,
RA Jones S.U., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN [12]
RP STRAIN=NMRI; TISSUE=Mammary tumor;
RC Strausberg R.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC047086; AAH47086.1; -.
DR HSSP; P18052; IYRO.
DR MGD; MGI:97809; Ptpdb.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR00387; TYR phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; FN3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PTPYPPHPTASE.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00853; FN3; 6.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT NON TER
SQ
SEQUENCE 1102 AA; 124677 MW; 8281DF729BP9148 CRC64;

Query Match 17.3%; Score 1219.5; DB 2; Length 1102;
Best Local Similarity 29.4%; Pred. No. 2.2e-60;
Matches 354; Conservative 197; Mismatches 455; Indels 199; Gaps 40;

QY 201 IKVTEPIPVSDRLVALTGR-KAALSMNGNTASGRVLSEIGHBELTQDSRLQVNI 259
DB 6 IEGLTVPSTYKNIHISANGATDRLMTWSPGG----- 38
QY 260 SLDKPGVQVNIINPYLLQSNKTKGDPLETEGLDASNTERRAGSPAPVHDSLVGPVDP 319
DB 39 -----DVDSVVSAPR-----QBEKVDQSQITPK----- 62
QY 320 SSGQGSRTPEVLVLGEPGRNATYVSOANETGQPOAIRTAIYQVDTAVN-IS 378
DB 63 -----ASHTHRLEAGAKRIATVS-VSGSLRNQIDALG-QTVPASQGVANAVS 113
QY 379 ATSLTLIMKVDNESSNYTKIHVAGETDSNLATYSEPPA-----VIRPLRSTPY 430
DB 114 SNLVTYSWQALGVAE---RYDILLNENGLLSNVSEFATARQHFEDLTREKK---Y 166
QY 431 NITVCPVLGDIETGPGLQVHTPPVPSDFRVTVSTTEIGLAWSSHDAESFQMI--T 487
DB 167 KMQILTVSGGLFSKESQAEGRTPAVALTNLIRITENSSRYLSFGWTASEGLSWNIFLYN 226
QY 488 QEAGNSRVEI-TTNSIIIGLFPGTKCFELVPGNPGTEGASTVCNRTVPSAVPI 546
DB 227 PDDTLDERKQVDPVLSVSFQNLQGRKRMVIVH--SGELSNESFIRGTVPAAVNH 284
QY 547 HVVYVTTT-MMLDMKSPGASERYVHYLVYESGNSHTSYDKAIT---LOGLIFG--- 599
DB 285 KSGHRTTTSLSWSPAGDPDF-YELLVNPNGKKNMKKOVTEMRPGVLVGRKY 343
QY 600 TLVNTITSEVDHVMGDNPSTQVTRPSNVSNIDVSTNTAATL---SWQNPDDAS--- 652
DB 344 TLVVVTHSDLSNKTVGBRGRTAP-SPPSILSFADVANTSLAITWKGPDMTDYDFELQW 402
QY 653 -PVSYCLIEKAGNSNATQVVTIDIGIDAVYTELIPSSYTVAFIAQVGGIKSL-EP 710
DB 403 FPDALTITNPVSRKSGE-----RIVYGLHPRSRQFSVKTVSGSWMTYSXP 451
QY 711 GRKSFCTDPAVASPDCEVVPKEPALVLKTCPPGANAGFELEVSAGAMNATHTLESQSS 770
DB 452 ISGSVATKDKQIONLHCR-PQNSTALACSWIPDSDPQGISL-----CRKMDTQEI 502
QY 771 ENGETRETEVYTLNF-----STSYNISITTVSGCKMAAPTRNTCTTGITDPPPDGSPNI 825

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Db      503 EFSKLEKESKLINIMLVPHKRYLVSIKVGSAGTSEVEDSTITMDREPQD--PPII 560
Qy      826 -----TSVHNSVK--VKPSGFASHPICAYAVILTTG-----EACHPADVLKY 869
Db      561 RVNEKDVLISSSINFTVNCSEWFSDTGAVYFVAVVAREADSMELKEPQHPSPYLEY 620
Qy      870 TYDDPFKGAADTYTYLIRTEEKRSQSLSEVLKYEIDVGNESITLG-----YYNG 920
Db      621 RHNASIRVQTN--FASKCAESPDSSKS-----FNIKLGEMSLGKCDPQOQKPCDG 674
Qy      921 KLEPLGSYRACVACFTNITTFHPQKGLDGAESYVSFSRYSDAVSLPDP--GVICGAVF 978
Db      675 PLKPHYAVIRISIRAFQTLF-----DEDLKEFTKPLYSDFPFMPITTEBEPFVGLGVSA 730
Qy      979 GCIFGALVITYVGFIFMRK--KKDKAKNEVSQSQIKP-----KSKLIRV 1023
Db      731 GLPLIGMLVAVLVAFFICRQKASHRSRPSARLSIRDRPLSVHLNLGQGNKRTSCPIKI 790
Qy      1024 ENFEAYFKQOQADNSCGFAEYEDLKLVGISQPKYAEIAENRGKRNRYNNVLPYDISRVK 1083
Db      791 NOFEGHFMKQADSNLYLSKEYEDLKDVGSQSCDIALLPENRGKRNRYNNVLPYDASRVK 850
Qy      1084 L-SYQTHSTDDYINANMPGYSHSKDFIATQGPLNTLKDPMRWVMEKNVYAIIMLTQCV 1142
Db      851 LCNVDVDDPCSDYINASYIPGNPFREYIATQGPLPTGMDPMKAMEQVANIWMVTCV 910
Qy      1143 ECGRTKCEBYWPSKQ-AQDYDDITVANTSEIVLEPWTIRDTVKNIGTSEHPL-RQHF 1200
Db      911 EKGKVKCDHWPADQDPLLYGDLILQWSESVLEPWTIRDKIASEBQDLHRLIRHPIY 970
Qy      1201 TSWPDHGVPTTDLINFRYLVRDYMKQSPESPILVHCSGVGRTGFIALIDRLIYOIE 1260
Db      971 TWPDPHGVPTTDLIOPFRVRYDIYINRSPAGFVHCSGVGRTGFIALIDRLIYOIE 1030
Qy      1261 NENTVDYGYVYDLRMHRLPMVQTEDOYVFLNQCULDIVRSQKSKVDLIYQNTAMTY 1320
Db      1031 SKDSVDIYGAVHDLRLRHVHVQTECGYVLYHQCVRDYLAKCLRN-----EQENPLFPIY 1086
Qy      1321 ENLAP 1325
Db      1087 ENVNP 1091

RESULT 14
Q9HD43 PRELIMINARY; PRT; 1115 AA.
ID Q9HD43 AC Q9HD43;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Transmembrane-type protein cytosine phosphatase H.
GN Name=PTPRH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21328879; PubMed=11435690;
RA Marnett A.G., Mehenni H., Reichenberger E., Antonarakis S.E.,
RA Krieg T., Olsen B.R.;
RT "Gene for the human transmembrane-type protein tyrosine phosphatase H
RT (PTPRH): genomic structure, fine-mapping and its exclusion as a
RT candidate for Pautz-Jeghers syndrome."
RL Cytogenet. Cell Genet. 92:213-216(2001).
DR EMBL: AF275130; AAF91411.1; -.
DR EMBL: AF275131; AAF91411.1; JOINED.
DR EMBL: AF275132; AAF91411.1; JOINED.
DR EMBL: AF275133; AAF91411.1; JOINED.
DR EMBL: AF275134; AAF91411.1; JOINED.
DR EMBL: AF275135; AAF91411.1; JOINED.
DR EMBL: AF275136; AAF91411.1; JOINED.

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DR EMBL: AF275137; AAF91411.1; JOINED.
DR EMBL: AF275138; AAF91411.1; JOINED.
DR EMBL: AF275139; AAF91411.1; JOINED.
DR EMBL: AF275140; AAF91411.1; JOINED.
DR EMBL: AF275141; AAF91411.1; JOINED.
DR EMBL: AF275142; AAF91411.1; JOINED.
DR EMBL: AF275143; AAF91411.1; JOINED.
DR EMBL: AF275144; AAF91411.1; JOINED.
DR EMBL: AF275145; AAF91411.1; JOINED.
DR EMBL: AF275146; AAF91411.1; JOINED.
DR EMBL: AF275147; AAF91411.1; JOINED.
DR EMBL: AF275148; AAF91411.1; JOINED.
DR EMBL: AF275149; AAF91411.1; JOINED.
DR HSSP: P18052; 1YFO.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016787; F: hydrolase activity; IEA.
DR GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN III-like.
DR InterPro: IPR000387; TYR phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; FN3; 7.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PTPYPPHPTASE.
DR SMART: SM00060; FN3; 7.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS50853; FN3; 7.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Transmembrane.
SQ
SEQUENCE 1115 AA; 122351 MW; A7A1AB24CFCD3846 CRC64;

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Query Match 16.7%; Score 1176.5; DB 2; Length 1115;
Best Local Similarity 26.3%; Pred. No. 6,3e-58;
Matches 366; Conservative 188; Mismatches 456; Indels 383; Gaps 43;

8 ARLPSPG-----LRNALPLLLLLLRGQLLCAGTSPSPIDPSAVATVAT 53
25 ARAPAPNPNRNLYETOTTSISLSWEVP-----DGLDS--QNSNYVQCT 68
54 GENGITQISSTAESFHKQNGTGPQVETNTSEDESSGA--NDSLRTPEQSGNGTDAQ 111
69 GDGTTETRNT-----TATNTVVDLGGPGLTGCVMWEKQVNSVGT-- 112
112 KTPSTGSPVFDIKAVSISPTNVLTKWSNDRTAASEYK-YVGHKNEK--TITVVHQ 168
113 -VTATAPNPNRNLRVAQTSSIALTWBEVDPGPQNSTYGVETGDPGAGTRSTAH- 170
169 PWCNIT--GLRPAVSYSITPGIGNETWGPRIYKIVTEPIPVSDLRVALTGVRKALS 226
171 -TNTVTDGLEPGLVAPSWVWG-KNGINSRETRNATTANPNRNLRVAQTSSISLS 227
227 WSNNGTASCRVLLSISGSHBELTQDSRLQVNSIDLKPGVQYNINPYLLQSNKTKGDP 286
228 WEVPDGT-----PQNS-----TYCVQCT-----G 247
287 TEGGLDASNTERSRAGSPFAVHDESLVGPVDPSSGQGRDTEVLLVGLERTYNATVY 346
248 DGRGTRTNT-----TDRTRVTVGLGSGSLYSCSVW 278
347 SQAANGTEGQQALETFTNMQVDTYAVNISA---TSLTILMKVSNSSNTYKIHV 403
279 VE----KGVNSVSEIYTSATAPNPNRNLYEAQTNSSIALTWBEVDPGPDPQNSTYGV 334
404 AGETDSNLINVSBRRAVYIPLGSLSTFYNTVCPIAGDIBGTGFLQVH----- 451
335 TGDGGR-----GTRSTAHNTITVDRL-----EPGLLYFVSVWVGKGINSS 376
452 -----TPPVSDFRVTVVSTTEIGLAWSHDAE-----SPQMHITQEGAGNSRVEIT 499
377 RETNATTAAPNPNRNLRVAQTSSIALCWEVDPGPVQDYTYWVEYTGDG--GGTETRNT 435

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QY 500 TNOGIIIGLPGRTKTCFELVPGKPNGTGASRTVCNRTPSAVPDHHVVTTEMD 559
DB 436 TMTSVTAERLEPGLTITFSVMAE-KNGARGSRONVSIIVPAVNTSLSQDMNTSTLAR 494
QY 560 WKSPD--GASEYTHL--VIESHGSHNTSTYDKATITLQGLIPGLYNTITSPEDHWG 615
DB 495 WTAPQGPQSSSYYSWYVSWREGMTDPRQTOSTGTDITLKELEAGSLYHLTWAEERVAG 554
QY 616 DPSTAQYRPSVNSINDVSTNTATLSMNF--DDAPYSYCLLIKAKN----- 666
DB 555 YNSTLRAAPNVTLONETQKNSVLMWKAPEGHSOLYYVWQWASKGHPRGODP 614
QY 667 SSNAIVTVDIGITDATTTELIPGSSYVEIPAQVGDGKISLEPGKSPC--TDPASMAS 724
DB 615 QANWVQTSRTMETWYKVALEBGLTYNFTWAERNDVASSTQ--SLCASTYDIYTI 670
QY 725 PDEVVVKEPALVLTCTCPGPNAGBELVSSGAMNATHLESCESENGETRYRTVYLN 784
DB 671 TSCVSTASAGVNLWSPQGGVEAFELV-----GQORSGSDRS----- 710
QY 785 FSTSYNISITTVSCGMAAPTRNTCTTGITDPPPDGSPNITSVSHNVKVFSGFEASH 844
DB 711 -----SCGEAVS-----VLGL----- 721
QY 845 GEIKAYAVILTTGEAGHSADVLTCTYDDPKKASDTYVYLIIRTEKRGSGSLSEVLKY 904
DB 722 GPARSPATIT-----IWDGK-----VYSH 743
QY 905 EIDVGNSTTLGYNGKLEPLGSYRACVAGFNITFHQNGKLDGASVYSFRTSYNAV 964
DB 744 SYVCHTESA----- 752
QY 965 SLDPDPGYICGAVFCIGALVITVGGPIFWKKRDKAKNNEVSFSQIKKESKL----- 1020
DB 753 -----GYIAGAFVGL--LEFLIVGLLIFLKRKNKK-----QKRELNDIVSS 796
QY 1021 ---IRVNEPAVFKQADNSNGFAEEYEDLKTIVGISPKYAAELAEKGRNNNTLPY 1077
DB 797 PGDIAPEDPADHVRKNERDSNGCFADKYQLSLVSHSQSOMVASSENNAKRYRNVLPY 856
QY 1078 DISRVKLS-VQTHSTDDYINANMPGVSKDFIATQGPLPNTLKDFRWMEKGVNVALI 1136
DB 857 DMSRVPLKPIHBEPSDYINASPMGLMSPEFIATQGPLQYTGDFRWMEQOSHLLV 916
QY 1137 MLTKVEGRTKCEYRP-SKQADYGDITYAMTSEIVLPWTIRDFVTXNIQTSSEHPL 1195
DB 917 MLTKMEGARKVCEHYWPLDSQPCFHGLRYTLVGEEMENWTVRELLILQVEBQKTLV 976
QY 1196 RQFHTSPDHGVPDITDLINFRILVADYWKOSPPSPILVHGSAGVGTGFIADRL 1255
DB 977 RQFHYQAMPDHGVSSPDTLLAFKRLKRWMLDQTMEGGPPIVHGSAGVGTGFIADVL 1036
QY 1256 IYQIENENTVDYGIYVDLRNHRPLMVTQEDQYVFLNQCVLDIVR--SQKDSKVDLIYQN 1313
DB 1037 LRQLOSSELLGPFSFVFRKMRRESRLMVTQEAQYVFLHQCLIRFLQQAQAPAEKEVYED 1096
QY 1314 TTAMTIYENLAPV 1326
DB 1097 VENL-IYENVAI 1108

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RESULT 15

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ID 015426 PRELIMINARY; PRT; 1118 AA.
AC 015426;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Protein tyrosine phosphatase precursor.
GN Name=5AP-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_taxid=9606;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=94124561; PubMed=8294459;
RA Matczaki T., Suzuki T., Uchida T., Inazawa J., Ariyama T., Matsuda K.,
RA Horita K., Noguchi H., Mizuno H., Sakamoto C., Kasuga M.;
RT "Molecular cloning of a human transmembrane-type protein tyrosine
RL phosphatase and its expression in gastrointestinal cancers.";
RL J. Biol. Chem. 269:2075-2081(1994).
DR EMBL; D15049; BA03645.1; -
DR PIR; A49724; A49724.
DR HSSP; P18052; 1YFO.
DR Gene; HGNC:9672; PTPR.
DR GO; GO:0005887; C:intracellular plasma membrane; TAS.
DR GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. .; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; Fns3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00853; FN3; 6.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR KEGG; K04101; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 1118 protein tyrosine phosphatase.
SQ SEQUENCE 1118 AA; 123038 MW; F73B3967BCES9F00 CRC64;

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Query Match 16.1%; Score 1130; DB 2; Length 1118;
Best Local Similarity 25.9%; Pred. No. 2; 7e-55;
Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

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QY 8 ARLPSPG-----LRALPLLLLRIGLILGAGGPPSPPTPVATVAT 53
DB 25 ARAPAPNPGRLNLTVEQTSSISLSWEV-----DGLDS--QNSNWQCT 68
QY 54 GENGITQISSIAESFKHNGKGTGPQVETNTSDESSGA--NDSLRTPQSGNGTDGASQ 111
DB 69 GIDGTEETENT-----TATNVTYDGGPSGLYCSVWVEKDGYNSSVGT-- 112
QY 112 KTPSSGSPSPVDIKAVSIPNVLITWKSNTTASSEK--YVYKAKMENK--TITVHQ 168
DB 113 -VTTATAPNPNKRLRVEAQNTSSIALTWEPDGPDPQNSTYGVETYGCGRAGTSTAH- 170
QY 169 PWCNIT--GLRPATSVFSPITPGIGNETWGDPRVILKITEPIPVSDLRVALTGVRKALS 226
DB 171 --TNITVDLBPGLIYAFSM----- 188
QY 227 WNGNGTASCRVLLESIGSHEELT---DSLQVINIDLKRGVQYINPNYLLQSNKTKG 282
DB 189 WVKNGINSSRETNATTAHNPVRKPRBSGSDHQLPEL--GGRPMH--RPTIELDLRTSA 246
QY 283 DPLGTEGCLDAENSTRSPRAGSPYAVHDESLVGPDPSPGGSQSRTEVLVLVLEPGTAYN 342
DB 247 LEMVAEGRLETOQTES-----PVD-----GLBGSLLT 275
QY 343 ATVYSGAANGTEGQPAIEFRTNALQVFDYAVNISATSLILWKSNDNESSVYTKIH 402
DB 276 CSVWVEKGVNSSSWRLVSTTAPNPVNLVFEAQNTSSIALTWEPDGPDPQNSTYGV 335
QY 403 VAGETDSSNLNWSSEBRAVYPLGRSFTNITVCPVLGIGESTPFLQYH----- 451
DB 336 YTGDDGRA-----GTRSTAHNTITVDRL-----EPCLVYFSVWVGKNGINS 377
QY 452 -----TPPVVSDFRVTVVSTTEIGLWSSHDAR-----SPQMIHIOGAGNSRYEI 498
DB 378 SRETNATTAHNPVRLNLMETQNTSSIALCWEVFDGPPQDYTYWVGITGDG--GGETRN 436

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